BS

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/815,242	03/21/2001	Robert Haselbeck	ELITRA.011A	7191

210 7590 11/17/2004

MERCK AND CO INC
P O BOX 2000
RAHWAY, NJ 070650907

EXAMINER	
GIBBS, TERRA C	

ART UNIT	PAPER NUMBER
1635	

DATE MAILED: 11/17/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/815,242	HASELBECK ET AL.	
	Examiner	Art Unit	
	Terra C. Gibbs	1635	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *29 December 2003*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-102* is/are pending in the application.

4a) Of the above claim(s) *1-11,13-30,32-44 and 70* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *12, 31, 45-69 and 71-102* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *November 17, 2003*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Attached sequence hit list*.

DETAILED ACTION

This Office Action is s response to Applicants Amendment and Remarks filed September 28, 2004.

Claims 1-102 are pending in the instant application. Claims 1-11, 13-30, 32-44 and 70 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement on June 30, 2002.

Claims 12, 31, 45-69, and 71-102 have been examined on the merits.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Change in Power of Attorney

Applicant's change in Power of Attorney filed September 28, 2004 is acknowledged.

Specification

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. Appropriate correction is required.

The lengthy specification has not been checked to the extent necessary to determine the presence of all possible minor errors. Applicant's cooperation is requested in correcting any error of which Applicant may become aware in the disclosure.

Withdrawal of Finality

Applicants received a Final Office Action mailed March 22, 2004. After careful reconsideration of the claims, the Examiner has decided to reopen prosecution of the instant application because 35 U.S.C. 112, first paragraph issues were not raised by the Examiner earlier during prosecution. The Final Office Action mailed March 22, 2004, is vacated and a new Non-Final Office Action on the merits follows.

Response to Arguments

In the previous Office Action mailed March 22, 2004, claims 12, 31, 45-69 and 71-102 were rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

In response to this rejection, Applicants argue that neither the independent claims, nor the claims dependent thereon, are drawn to an invention that encompasses "*any gene* product in a cell whose activity is reduced by an antisense, thereby producing a sensitized cell", as argued by the Examiner. Applicants contend that the claims are drawn to providing an antisense nucleic acid to reduce the activity or amount of a gene product whose activity or amount is reduced by an antisense comprising a nucleotide sequence having a specific sequence identification number, namely elected SEQ ID NO:1463. Applicants also argue that the specification describes several yphC genes from a variety of cells, the gene products encoded by those genes, and antisense nucleic acids that are capable of reducing the activity or amount of such yphC gene product.

Applicants argue that this description is in accordance with the Written Description Guidelines (66 FR 1099, January 5, 2001).

Applicant's arguments have been fully considered and are found persuasive by the Examiner. Specifically, the Examiner agrees that the claims are drawn to providing an antisense nucleic acid to reduce the activity or amount of a gene product whose activity or amount is reduced by an antisense comprising a nucleotide sequence having a specific sequence identification number, namely elected SEQ ID NO:1463. The Examiner has also been persuaded by Applicants Remarks regarding that the specification describes several yphC genes from a variety of cells, the gene products encoded by those genes, and antisense nucleic acids that are capable of reducing the activity or amount of such yphC gene product. Therefore, in view of Applicants arguments, the 35 U.S.C. 112, first paragraph rejection against claims 12, 31, 45-69 and 71-102 for written description is withdrawn.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 12, 31, 45-69, and 71-102 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. **This is a written description rejection.**

Applicant is referred to the interim guidelines on written description published on December 21, 1999 in the Federal Register at Volume 64, Number 244, pp. 71427-71440.

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the 'written description' inquiry, whatever is now claimed." (see page 1117). The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invention what is claimed." (See Vas-Cath at page 1116).

The specification provides adequate written description for a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid comprising SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing sensitized bacterial cells, as described in claims 101 and 102.

However, the claims are so broad as to encompass producing *any* type of sensitized cell, including cells from higher organisms. A sequence search of the relevant art reveals that SEQ ID NO:1463 is an antisense nucleic acid 100% complementary to the YphC gene of the *Staphylococcus aereus* bacterium (see attached sequence hit list). It is noted that the prior art hit list reflects only microbial cells, and not higher organisms. Applicant's arguments, filed December 29, 2003 describe the YphC gene as being required for proliferation of *Staphylococcus auerus* (see Applicants Remarks, page 2, first paragraph). It appears that the prior art and Applicants Remarks filed December 29, 2003 describe that SEQ ID NO:1463 will only target and sensitize bacterial cells, as opposed to *any* cell, including cells from higher

organisms as broadly claimed. The species specifically disclosed is not representative of the genus because the genus is highly variant (e.g. protista cell, bacterial cell, fungal cell, plant cell, animal cell, etc.). Given the broadness of the sensitized cell encompassed in the claimed methods, the disclosure of the specification provides insufficient written description to support the genus encompassed by the claim.

Claims 31, 45-69, 71-84, and 102 are drawn to a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid having at least 97%, 95%, 90% 85%, 80%, 70% sequence identity to SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized cell.

The specification as filed teaches providing a sublethal level of an antisense nucleic acid comprising SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized bacterial cell, as described in claims 101 and 102. The specification as filed fails to adequately describe providing a sublethal level of an antisense nucleic acid having at least 97%, 95%, 90% 85%, 80%, 70% sequence identity to SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized cell.

With limited disclosure provided by the specification, the skilled artisan cannot envision those antisense nucleic acids with varying degrees of sequence identity to SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized cell. This functional limitation itself is not sufficient to provide a structure/function relationship for meeting the written description requirement because it is not clear what structure

the antisense nucleic acids with varying degrees of sequence identity to SEQ ID NO:1463 would have by the recitation of the functionality alone, "reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized cell". The specification provides no guidance in this regard. The claimed invention as a whole is not adequately described if the claims require essential or critical elements which are not adequately described in the specification. Possession may be shown by actual reduction to practice, clear depiction of the invention in a detailed drawing, or by describing the invention with sufficient relevant identifying characteristics such that a person skilled in the art would recognize that the inventor had possession of the claimed invention. *Pfaff vs. Electronics, Inc.*, 48 USPQ2d, 1641, 1646 (1998).

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481, 1483. In Fiddes, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid comprising SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing sensitized bacterial cells, as described in claims 101 and 102, meets the written description provision of 35 U.S.C. 112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. 112 is severable from its enablement provision (see page 1115).

Claims 12, 31, 45-69, and 71-102 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid comprising SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized bacterial cell as described in claims 101 and 102, does not reasonably provide enablement for a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid comprising SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing *any* sensitized cell, as recited in claims 12 and 85-100, or a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid having at least 97%, 95%, 90% 85%, 80%, 70% sequence identity to SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized cell, as recited in claim 31 and 45-84. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or the invention commensurate in scope with these claims. **This is a scope enablement rejection.**

The following factors have been considered in formulating this rejection (*In re Wands*, 858F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988)): the breadth of the claims, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, the amount of direction or guidance presented, the presence or absence of working examples of the invention, and the quantity of experimentation necessary.

Claims 12 and 85-101 are drawn to a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid comprising SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing *any* sensitized cell. Claims 31, 45-84, and 102 are drawn to a method for screening a candidate compound for the ability to reduce cellular proliferation comprising providing a sublethal level of an antisense nucleic acid having at least 97%, 95%, 90% 85%, 80%, 70% sequence identity to SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized cell.

To begin, as per the 35 U.S.C. 112 first paragraph rejection above for written description, there is no direction or guidance in the instant specification as filed for producing *any* sensitized cell, other than those bacterial cells described in claims 101 and 102. For example, what kind of cell will have the target for SEQ ID NO:1463 encoding a gene product whose activity or amount is reduced such that the cell is sensitized? A sequence search of the relevant art reveals that SEQ ID NO:1463 is an antisense nucleic acid 100% complementary to the YphC gene of the *Staphylococcus aereus* bacterium (see attached sequence hit list). It is noted that the prior art hit list reflects only microbial cells, and not higher organisms. Applicant's arguments, filed December 29, 2003 describe the YphC gene as being required for proliferation of *Staphylococcus auerus* (see Applicants Remarks, page 2, first paragraph). It appears that the prior art and Applicants Remarks filed December 29, 2003 describe that SEQ ID NO:1463 will only target and sensitize bacterial cells, as opposed to *any* cell, including cells from higher organisms as broadly claimed. Significant trial and error experimentation would be required to practice the method over the scope claimed since the skilled artisan would need to determine

what kind of cell (e.g. protista, bacterial, fungal, plant, animal, etc.) will have the target for SEQ ID NO:1463 encoding a gene product whose activity or amount is reduced such that the cell is sensitized, and serve to screen for candidate compounds which inhibit proliferation. There is no predictability whether *any* kind of sensitized cell can be produced by the methods recited, other than those bacterial cells described in claims 101 and 102.

Second, and as per the 35 U.S.C. 112 first paragraph rejection above for written description, there is no direction or guidance in the instant specification as filed for providing a sublethal level of an antisense nucleic acid having at least 97%, 95%, 90% 85%, 80%, 70% sequence identity to SEQ ID NO:1463, which reduces the activity of a gene product required for cellular proliferation, thereby producing a sensitized bacterial cell. The specification teaches SEQ ID NO:1463, which reduces the activity of a gene product, thereby producing a sensitized bacterial cell as described in claims 101 and 102. The specification as filed fails to adequately describe those antisense nucleic acids with varying degrees of sequence identity to SEQ ID NO:1463, which produces a sensitized cell. Because functionality alone as recited in the instant claims does not elucidate the structure (e.g. nucleotide sequence) it would require undue experimentation to practice the invention as claimed. The quantity of experimentation required to practice the invention as claimed would involve the determination of those antisense nucleic acids with varying degrees of sequence identity to SEQ ID NO:1463, which reduces the activity of a gene product, thereby producing a sensitized cell. To practice the claimed methods, the skilled artisan would need to undergo undue trial and error experimentation, beyond the teachings and guidance of the specification to practice the methods, over the scope claimed.

Therefore, in view of the unpredictability of the art, the breadth of the claims, and the lack of guidance provided by the specification, one of ordinary skill in the art at the time of the invention would have required an undue amount of experimentation to make and use the claimed invention over the scope claimed.

Conclusion

No claims are allowable.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Terra C. Gibbs whose telephone number is (571) 272-0758. The examiner can normally be reached on M-F 9:00-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John L. LeGuyader can be reached on (571) 272-0760. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

tcg
November 4, 2004

JOHN L. LeGUYADER
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Applicants Copy
Sequence Hit List

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 17:16:39 ; Search time 129.915 Seconds
(without alignments)
8041.284 Million cell updates/sec

Title: US-09-815-242-1463
Perfect score: 387
Sequence: 1 gatcttcttcctcttcacca.....ttcacctgaagaataaatac 387

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		387	100.0	387	23	AAS48886	Staphylococcus aur
c 2		387	100.0	1311	22	AAF86461	Staphylococcus aur
c 3		387	100.0	1311	23	AAS54997	Staphylococcus aur
c 4		383.8	99.2	1305	23	AAS51646	Staphylococcus aur
c 5		383.8	99.2	1311	23	AAS54865	Staphylococcus aur
c 6		327	84.5	3621	18	AAV74669	Staphylococcus aur
7		295	76.2	372	23	AAS50706	Staphylococcus aur
c 8		262.2	67.8	1332	24	ABN90883	Staphylococcus epi
9		262.2	67.8	3269	22	AAH54708	S. epidermidis gen
10		234	60.5	298	23	AAS50205	Staphylococcus aur
11		234	60.5	298	23	AAS50723	Staphylococcus aur
c 12		205.8	53.2	319630	24	ABQ67194	Listeria innocua c
13		205.8	53.2	2944528	24	ABA03041	Listeria monocytog
14		205.8	53.2	3011208	24	ABQ69245	Listeria innocua D
c 15		174.4	45.1	1311	24	ABK75008	Bacillus lichenifo
c 16		162.6	42.0	1308	24	ABN68458	Streptococcus poly
c 17		162.6	42.0	2365589	24	ABA90521	Genomic sequence o
c 18		160.4	41.4	1308	24	ABN68457	Streptococcus poly
19		160.4	41.4	2155561	24	ABN71527	Streptococcus poly
c 20		153	39.5	1311	21	AAA54516	yphC gene of Strep
c 21		151.4	39.1	1308	25	ABX07474	S. pneumoniae type
c 22		151.4	39.1	1311	21	AAZ91826	Streptococcus pneu
23		151.4	39.1	5066	19	AAV52212	Streptococcus pneu
24		151.4	39.1	2162598	25	ABS56454	Streptococcus pneu
25		146	37.7	246	23	AAS49268	Staphylococcus aur
c 26		101	26.1	960	22	AAH53683	S. epidermidis ope
c 27		89.4	23.1	1512	23	AAS52517	E. coli DNA for ce
28		89.4	23.1	11574	22	AAS46244	DNA encoding novel
29		86	22.2	157	23	AAS50894	Staphylococcus aur
c 30		84.4	21.8	1512	22	AAF94379	Haemophilus influe
c 31		84.4	21.8	1512	24	ABK64943	DNA encoding Haemo
c 32		84.4	21.8	1515	23	AAS53235	Haemophilus influe
c 33		83.8	21.7	1473	23	AAS55968	Salmonella typhi D
34		80.6	20.8	640681	24	ABA92787	Buchnera sp. genom
35		80.2	20.7	1830121	17	AAT42063	Haemophilus influe
36		73.2	18.9	1370	19	AAZ96377	S. pneumoniae deri
c 37		73	18.9	33140	22	AAF28536	Genomic fragment #
c 38		69.8	18.0	1146	25	ACA00899	C. glutamicum deri
c 39		69.8	18.0	1557	22	AAH66542	C glutamicum codin
c 40		69.8	18.0	349980	22	AAH68528	C glutamicum codin
c 41		69.8	18.0	349980	22	AAH68529	C glutamicum codin
42		64	16.5	25360	22	AAF88314	S. spinosa DNA fra
43		64	16.5	29736	22	AAF88317	S. spinosa DNA fra
44		62	16.0	580073	18	AAT58840	Mycoplasma genital
c 45		61.4	15.9	78845	21	AAA81463	N. meningitidis pa

ALIGNMENTS

RESULT 1
AAS48886
ID AAS48886 standard; DNA; 387 BP.
XX
AC AAS48886;
XX
DT 13-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation inhibitory sequence #110.
XX
KW Antisense; ss; prokaryotic cellular proliferation;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX

```
PI   Haselbeck R,  Ohlsen KL,  Zyskind JW,  Wall D,  Trawick JD,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2001-611495/70.
XX
PT   New polynucleotides for the identification and development of
PT   antibiotics, comprise sequences of antisense nucleic acids -
XX
PS   Claim 1; Seq ID No 1463; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the
CC   genes, their use in the discovery of novel antibiotics, the essential
CC   genes themselves and the encoded proteins. The prokaryotes used are
CC   Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC   invention is also useful for the identification of potential new targets
CC   for antibiotic development. The antisense nucleic acids can also be used
CC   to identify proteins used in proliferation, to express these proteins,
CC   and to obtain antibodies capable of binding to the expressed proteins.
CC   The proteins can be used to screen compounds in rational drug discovery
CC   programmes. The antisense nucleic acid sequence is also useful to screen
CC   for homologous nucleic acids which are required for cell proliferation in
CC   a wide variety of organisms. The present sequence is an antisense
CC   oligonucleotide of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 387 BP; 122 A; 91 C; 53 G; 121 T; 0 other;

  Query Match             100.0%;  Score 387;  DB 23;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-98;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              |||||||||||||||||||||||||||
Db        361 TTAACCATTCACCTGAAGAATAAATAC 387


RESULT 2
AAF86461/C
ID   AAF86461 standard; DNA; 1311 BP.
XX
AC   AAF86461;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Staphylococcus aureus YphC coding sequence.
XX
KW   YphC; antimicrobial; cytostatic; antiulcer; microbial infection;
KW   gene therapy; vaccine; gastrointestinal carcinoma; gastric ulcer;
KW   gastritis; ds.
XX
OS   Staphylococcus aureus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1311
FT                   /*tag= a
FT                   /product= "Staphylococcus aureus YphC protein"
XX
PN   WO200123418-A1.
XX
PD   05-APR-2001.
XX
PF   19-SEP-2000; 2000WO-US25566.
XX
PR   28-SEP-1999;   99US-0406968.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Zalacain M,  Biswas S,  Burnham MKR,  Sylvester D,  Mcdevitt D;
PI   Mathie TB;
XX
DR   WPI; 2001-308138/32.
DR   P-PSDB; AAB82089.
XX
PT   Novel yphC polypeptides of Staphylococcus aureus useful for diagnosing
PT   and treating microbial infections, especially infection by
PT   Staphylococcus aureus and Helicobacter pylori -
XX
PS   Claim 2; Page 2-3; 41pp; English.
XX
CC   The present sequence is the gene encoding yphC polypeptide of
CC   Staphylococcus aureus. The yphC coding sequence and protein are useful
CC   for treating and diagnosing microbial infections such as infection caused
CC   by S.aureus and Helicobacter pylori. In addition, the yphC coding
CC   sequence and protein are useful for treating diseases such as
CC   H.pylori-induced cancers, e.g. gastrointestinal carcinoma, gastric
CC   ulcers, and gastritis. The present sequence was obtained from a library
CC   of clones of chromosomal DNA of S.aureus in E.coli. The sequencing data
CC   from two or more clones comprising overlapping S.aureus DNAs was used to
CC   construct the present contiguous DNA sequence.
XX
SQ   Sequence 1311 BP; 451 A; 184 C; 278 G; 398 T; 0 other;

  Query Match             100.0%;  Score 387;  DB 22;  Length 1311;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-98;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 449

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 389

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 329

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 269

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 209
```

```
Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 149

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              |||||||||||||||||||||||||||
Db        148 TTAACCATTCACCTGAAGAATAAATAC 122
```

RESULT 3
AAS54997/c
ID AAS54997 standard; DNA; 1311 BP.
XX
AC AAS54997;
XX
DT 13-FEB-2002 (first entry)
XX
DE Staphylococcus aureus DNA for cellular proliferation protein #1309.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU37138.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 8634; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1311 BP; 452 A; 184 C; 278 G; 397 T; 0 other;

```
  Query Match           100.0%;  Score 387;  DB 23;  Length 1311;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-98;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 449

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 389

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 329

Qy        181 ATTTGTATAAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATTTGTATAAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 269

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 209

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 149

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              |||||||||||||||||||||||||||
Db        148 TTAACCATTCACCTGAAGAATAAATAC 122
```

RESULT 4
AAS51646/c
ID AAS51646 standard; DNA; 1305 BP.
XX
AC AAS51646;
XX
DT 13-FEB-2002 (first entry)
XX
DE Staphylococcus aureus DNA for cellular proliferation protein #63.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU33787.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX

```
PS   Claim 27; Seq ID No 4228; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the
CC   genes, their use in the discovery of novel antibiotics, the essential
CC   genes themselves and the encoded proteins. The prokaryotes used are
CC   Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC   invention is also useful for the identification of potential new targets
CC   for antibiotic development. The antisense nucleic acids can also be used
CC   to identify proteins used in proliferation, to express these proteins,
CC   and to obtain antibodies capable of binding to the expressed proteins.
CC   The proteins can be used to screen compounds in rational drug discovery
CC   programmes. The antisense nucleic acid sequence is also useful to screen
CC   for homologous nucleic acids which are required for cell proliferation in
CC   a wide variety of organisms. The present sequence encodes an
CC   essential prokaryotic cellular proliferation protein.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1305 BP; 447 A; 181 C; 277 G; 400 T; 0 other;

  Query Match             99.2%;  Score 383.8;  DB 23;  Length 1305;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-97;
  Matches  385;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 449

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        448 AACCATGTGACCCTGATATTGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 389

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 329

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 269

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 209

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 149

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||| ||||||||||||||||||
Db        148 TTAACCACTCACCTGAAGAATAAATAC 122


RESULT 5
AAS54865/c
ID   AAS54865 standard; DNA; 1311 BP.
XX
AC   AAS54865;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Staphylococcus aureus DNA for cellular proliferation protein #1177.
XX
KW   Antisense; ds; prokaryotic cellular proliferation gene;
KW   antibiotic; antibacterial; drug design.
XX
OS   Staphylococcus aureus.
XX
PN   WO200170955-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US09180.
XX
PR   21-MAR-2000; 2000US-191078P.
PR   23-MAY-2000; 2000US-206848P.
PR   25-MAY-2000; 2000US-207727P.
PR   23-OCT-2000; 2000US-242578P.
PR   27-NOV-2000; 2000US-253625P.
PR   22-DEC-2000; 2000US-257931P.
PR   16-FEB-2001; 2001US-269308P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Haselbeck R,  Ohlsen KL,  Zyskind JW,  Wall D,  Trawick JD,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2001-611495/70.
DR   P-PSDB; AAU37006.
XX
PT   New polynucleotides for the identification and development of
PT   antibiotics, comprise sequences of antisense nucleic acids -
XX
PS   Claim 27; Seq ID No 8502; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the
CC   genes, their use in the discovery of novel antibiotics, the essential
CC   genes themselves and the encoded proteins. The prokaryotes used are
CC   Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC   invention is also useful for the identification of potential new targets
CC   for antibiotic development. The antisense nucleic acids can also be used
CC   to identify proteins used in proliferation, to express these proteins,
CC   and to obtain antibodies capable of binding to the expressed proteins.
CC   The proteins can be used to screen compounds in rational drug discovery
CC   programmes. The antisense nucleic acid sequence is also useful to screen
CC   for homologous nucleic acids which are required for cell proliferation in
CC   a wide variety of organisms. The present sequence encodes an
CC   essential prokaryotic cellular proliferation protein.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1311 BP; 451 A; 181 C; 277 G; 402 T; 0 other;

  Query Match             99.2%;  Score 383.8;  DB 23;  Length 1311;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-97;
  Matches  385;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 449

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        448 AACCATGTGACCCTGATATTGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 389

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 329

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 269

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 209

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 149

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||| ||||||||||||||||||||
Db        148 TTAACCACTCACCTGAAGAATAAATAC 122


RESULT 6
AAV74669/c
ID   AAV74669 standard; DNA; 3621 BP.
XX
AC   AAV74669;
XX
DT   16-MAR-1999  (first entry)
XX
DE   Staphylococcus aureus contig SEQ ID #358.
XX
KW   Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW   cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW   skin infection; surgical wound infection; scalded skin syndrome;
KW   toxic shock syndrome; ds.
XX
OS   Staphylococcus aureus.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    481..540
FT                   /*tag= a
FT                   /note= "these bases represent a line of missing text in
FT                          the sequence listing in the specification. They
FT                          are included to maintain the nucleotide numbering
FT                          given in the specification for this DNA sequence"
FT   misc_feature    2281..2340
FT                   /*tag= b
FT                   /note= "these bases represent a line of missing text in
FT                          the sequence listing in the specification. They
FT                          are included to maintain the nucleotide numbering
FT                          given in the specification for this DNA sequence"
XX
PN   EP786519-A2.
XX
PD   30-JUL-1997.
XX
PF   07-JAN-1997;   97EP-0100117.
XX
PR   05-JAN-1996;   96US-0009861.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Barash SC,  Choi GH,  Dillon PJ,  Fannon MR,  Kunsch CA;
PI   Rosen CA;
XX
DR   WPI; 1997-374922/35.
XX
PT   Polynucleotide(s) and proteins derived from Staphylococcus aureus
PT   stored on computer readable medium and used in the production of
PT   anti-S.aureus vaccines
XX
PS   Claim 1; Page 1241-1243; 3271pp; English.
XX
CC   This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC   of the invention. The DNA sequences are recorded on a computer readable
CC   medium, preferably selected from a floppy or hard disk, random access
CC   memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC   the S.aureus DNA sequences allows putative functions to be assigned so
CC   that protein-encoding or regulatory regions of commercial, therapeutic or
CC   industrial importance can be obtained. Specifically, sequences which are
CC   likely to encode antigens have been identified and these polypeptides can
CC   be used in a vaccine composition against S.aureus infection. The
CC   polypeptides can also be used in a kit for the immunodetection of
CC   S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC   including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC   skin and surgical wound infections, scalded skin syndrome, toxic shock
CC   syndrome, etc. Organisms transformed with the DNA sequences can be used
CC   for recombinant production of the polypeptides. The new DNA sequences
CC   (and their fragments) are useful as primers or probes for isolating
CC   homologues of any of the S.aureus DNA sequences contained on the
CC   computer readable medium.
XX
SQ   Sequence 3621 BP; 1279 A; 442 C; 692 G; 1085 T; 123 other;

  Query Match             84.5%;  Score 327;  DB 18;  Length 3621;
  Best Local Similarity   84.5%;  Pred. No. 1.6e-81;
  Matches  327;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2637 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 2578

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2577 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 2518

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2517 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 2458

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2457 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 2398

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2397 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTNNN 2338

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
                                                                      |||
Db       2337 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTG 2278

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||||||||||||||||||||||||
Db       2277 TTAACCATTCACCTGAAGAATAAATAC 2251


RESULT 7
AAS50706
ID   AAS50706 standard; DNA; 372 BP.
XX
AC   AAS50706;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Staphylococcus aureus cellular proliferation inhibitory sequence #1930.
XX
KW   Antisense; ss; prokaryotic cellular proliferation;
KW   antibiotic; antibacterial; drug design.
XX
OS   Staphylococcus aureus.
XX
PN   WO200170955-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US09180.
XX
PR   21-MAR-2000; 2000US-191078P.
PR   23-MAY-2000; 2000US-206848P.
PR   26-MAY-2000; 2000US-207727P.
PR   23-OCT-2000; 2000US-242578P.
PR   27-NOV-2000; 2000US-253625P.
PR   22-DEC-2000; 2000US-257931P.
PR   16-FEB-2001; 2001US-269308P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Haselbeck R,  Ohlsen KL,  Zyskind JW,  Wall D,  Trawick JD,  Carr GJ;
```

```
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2001-611495/70.
XX
PT   New polynucleotides for the identification and development of
PT   antibiotics, comprise sequences of antisense nucleic acids -
XX
PS   Claim 1; Seq ID No 3283; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the
CC   genes, their use in the discovery of novel antibiotics, the essential
CC   genes themselves and the encoded proteins. The prokaryotes used are
CC   Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC   invention is also useful for the identification of potential new targets
CC   for antibiotic development. The antisense nucleic acids can also be used
CC   to identify proteins used in proliferation, to express these proteins,
CC   and to obtain antibodies capable of binding to the expressed proteins.
CC   The proteins can be used to screen compounds in rational drug discovery
CC   programmes. The antisense nucleic acid sequence is also useful to screen
CC   for homologous nucleic acids which are required for cell proliferation in
CC   a wide variety of organisms. The present sequence is an antisense
CC   oligonucleotide of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 372 BP; 113 A; 83 C; 51 G; 125 T; 0 other;

  Query Match             76.2%;  Score 295;  DB 23;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 7e-73;
  Matches  295;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          93 CCAAATCCTAATGAATAGAAATCATACACGTCTGTACGCATTTCCATATTATCTACTTTG 152
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 CCAAATCCTAATGAATAGAAATCATACACGTCTGTACGCATTTCCATATTATCTACTTTG 60

Qy         153 TTAACCGCTAATACGACCGGTTTTTTAGATTTGTATAAAATTTGAGCGACCATTTCATCG 212
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TTAACCGCTAATACGACCGGTTTTTTAGATTTGTATAAAATTTGAGCGACCATTTCATCG 120

Qy         213 CTTTGTGTCAATCCTTCACGCACGTTAACCATAAAAATAATAACATCCGCTTCATCTATG 272
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CTTTGTGTCAATCCTTCACGCACGTTAACCATAAAAATAATAACATCCGCTTCATCTATG 180

Qy         273 GCGATTTCTGCCTGCGCTCTAATTTGTGTTTGGAATGGTGCATCACCAATTTCAATACCA 332
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GCGATTTCTGCCTGCGCTCTAATTTGTGTTTGGAATGGTGCATCACCAATTTCAATACCA 240

Qy         333 CCTGTATCAATAATATTGAAATCATGTGTTAACCATTCACCTGAAGAATAAATAC 387
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CCTGTATCAATAATATTGAAATCATGTGTTAACCATTCACCTGAAGAATAAATAC 295


RESULT 8
ABN90883/c
ID   ABN90883 standard; DNA; 1332 BP.
XX
AC   ABN90883;
XX
DT   24-JUL-2002  (first entry)
XX
DE   Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:346.
XX
KW   Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW   antibacterial; gene therapy; gene; ds.
XX
OS   Staphylococcus epidermidis.
XX
PN   US6380370-B1.
XX
PD   30-APR-2002.
XX
PF   13-AUG-1998;   98US-0134001.
XX
PR   14-AUG-1997;   97US-055779P.
PR   08-NOV-1997;   97US-064964P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Doucette-Stamm LA,  Bush D;
XX
DR   WPI; 2002-381255/41.
DR   P-PSDB; ABP38338.
XX
PT   Novel isolated nucleic acid encoding a Staphylococcus epidermidis
PT   polypeptide, useful for diagnosing and treating bacterial infections -
XX
PS   Disclosure; SEQ ID 346; 267pp; English.
XX
CC   ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC   frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC   given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC   antibacterial activity and can be used in gene therapy. The sequences
CC   can also be used in the diagnosis and treatment of bacterial infections,
CC   particularly S. epidermidis infections. The sequences can be used to
CC   screen for compounds able to interfere with the S. epidermidis life
CC   cycle or inhibit S. epidermidis infection.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the
CC   USPTO web site.
XX
SQ   Sequence 1332 BP; 465 A; 190 C; 267 G; 410 T; 0 other;

  Query Match             67.8%;  Score 262.2;  DB 24;  Length 1332;
  Best Local Similarity   79.8%;  Pred. No. 1.6e-63;
  Matches  309;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy           1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
               ||||||||   |||| |  ||| |    ||||||||||||||| ||| || ||||| ||||
Db         529 GATCTTCTGATTCTTTATTAAAGTTTTCAACAACTGCATCTAGCAAATCTCCAAGTCCTA 470

Qy          61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
               | |||||||| || || || ||||| || || ||||| ||||| ||||||||||||| |
Db         469 ATCCATGTGAACCAGAAATAGGATATGGATCTCCAAAGCCTAAAGAATAGAAATCATAGA 410

Qy         121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
                 ||  |||||||||| | |||||| |||| || || |||||||| || ||||| ||||
Db         409 TATCATTACGCATTTCAAGATTATCAACTTTATTCACAGCTAATACAACAGGTTTCTTAG 350

Qy         181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
               |||| || |  ||||| |||||||||||| || |||||||| | |||||| |  || || |
Db         349 ATTTATAAAGCATTTGTGCGACCATTTCGTCACTTTGTGTAAGTCCTTCTCTAACATTGA 290

Qy         241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
               |||||||||| ||||| ||||| || || || ||||||||||| || |  ||||| |
Db         289 CCATAAAAATGATGACATCTGCTTCTTCAATTGCTATTTCTGCCTGTGCACGGATTTGAG 230

Qy         301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
               |||| || || ||||| |||||||||||||||||||||||||| || || || ||||| |
Db         229 TTTGAAAAGGAGCATCTCCAATTTCAATACCACCTGTATCAATGATGTTAAATTCATGAG 170

Qy         361 TTAACCATTCACCTGAAGAATAAATAC 387
               ||||||| || || || ||||||||||
Db         169 TTAACCACTCGCCAGATGAATAAATAC 143


RESULT 9
AAH54708
ID   AAH54708 standard; DNA; 3269 BP.
XX
AC   AAH54708;
XX
DT   03-SEP-2001  (first entry)
```

```
XX
DE   S. epidermidis genomic polynucleotide sequence SEQ ID NO:4072.
XX
KW   Staphylococcus epidermidis SR1 strain; infection; diagnosis;
KW   vaccination; endocarditis; ds.
XX
OS   Staphylococcus epidermidis.
XX
PN   WO200134809-A2.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US30782.
XX
PR   09-NOV-1999;   99US-0164258.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Kimmerly WJ;
XX
DR   WPI; 2001-316495/33.
XX
PT   Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT   useful for vaccinating against infections, e.g. endocarditis -
XX
PS   Claim 8; Page 1757-1759; 2188pp; English.
XX
CC   AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC   (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC   (I) and (II) can have antibacterial activity and therefore can be used
CC   in vaccination. The nucleic acids (I) may be used to produce the
CC   S. epidermidis polypeptides (II) via the production of vectors
CC   containing them which are used to produce hosts cells which express the
CC   polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC   used to vaccinate subjects and to raise antibodies against the bacteria.
CC   The polypeptides may also be used to assay for other inhibitors of their
CC   activity and therefore identify compounds that may be used for the
CC   treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC   AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC   polynucleotide sequences from the present invention. AAH55091 to
CC   AAH55098 represent oligonucleotide sequences and primers which are used
CC   in the exemplification of the present invention.
CC   N.B. The present invention specifically claims all the polynucleotide
CC   sequences given in the sequence listing of the present specification,
CC   however the sequence listing only goes up to SEQ ID NO:4454 so even
CC   though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC   no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ   Sequence 3269 BP; 986 A; 616 C; 451 G; 1216 T; 0 other;

  Query Match             67.8%;  Score 262.2;  DB 22;  Length 3269;
  Best Local Similarity   79.8%;  Pred. No. 2.1e-63;
  Matches  309;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||   |||| |  ||| |    ||||||||||||||| ||| || ||||| ||||
Db       2297 GATCTTCTGATTCTTTATTAAAGTTTTCAACAACTGCATCTAGCAAATCTCCAAGTCCTA 2356

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              | |||||||| || || || ||||| || || ||||| ||||| ||||||||||||||| |
Db       2357 ATCCATGTGAACCAGAAATAGGATATGGATCTCCAAAGCCTAAAGAATAGAAATCATAGA 2416

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
               ||  |||||||||| | |||||| ||||| || || |||||||| || ||||| ||||
Db       2417 TATCATTACGCATTTCAAGATTATCAACTTTATTCACAGCTAATACAACAGGTTTCTTAG 2476

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              |||| || |  ||||| |||||||||| || |||||||| | ||||||  |  || || |
Db       2477 ATTTATAAAGCATTTGTGCGACCATTTCGTCACTTTGTGTAAGTCCTTCTCTAACATTGA 2536

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              |||||||||| || ||||| ||||| || || || |||||||||| || |  ||||| |
Db       2537 CCATAAAAATGATGACATCTGCTTCTTCAATTGCTATTTCTGCCTGTGCACGGATTTGAG 2596

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              |||| || || ||||| |||||||||||||||||||||||||| || || || ||||| |
Db       2597 TTTGAAAAGGAGCATCTCCAATTTCAATACCACCTGTATCAATGATGTTAAATTCATGAG 2656

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||| || || || ||||||||||
Db       2657 TTAACCACTCGCCAGATGAATAAATAC 2683


RESULT 10
AAS50205
ID   AAS50205 standard; DNA; 298 BP.
XX
AC   AAS50205;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Staphylococcus aureus cellular proliferation inhibitory sequence #1429.
XX
KW   Antisense; ss; prokaryotic cellular proliferation;
KW   antibiotic; antibacterial; drug design.
XX
OS   Staphylococcus aureus.
XX
PN   WO200170955-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US09180.
XX
PR   21-MAR-2000; 2000US-191078P.
PR   23-MAY-2000; 2000US-206848P.
PR   26-MAY-2000; 2000US-207727P.
PR   23-OCT-2000; 2000US-242578P.
PR   27-NOV-2000; 2000US-253625P.
PR   22-DEC-2000; 2000US-257931P.
PR   16-FEB-2001; 2001US-269308P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Haselbeck R,  Ohlsen KL,  Zyskind JW,  Wall D,  Trawick JD,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2001-611495/70.
XX
PT   New polynucleotides for the identification and development of
PT   antibiotics, comprise sequences of antisense nucleic acids -
XX
PS   Claim 1; Seq ID No 2782; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the
CC   genes, their use in the discovery of novel antibiotics, the essential
CC   genes themselves and the encoded proteins. The prokaryotes used are
CC   Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC   invention is also useful for the identification of potential new targets
CC   for antibiotic development. The antisense nucleic acids can also be used
CC   to identify proteins used in proliferation, to express these proteins,
CC   and to obtain antibodies capable of binding to the expressed proteins.
CC   The proteins can be used to screen compounds in rational drug discovery
CC   programmes. The antisense nucleic acid sequence is also useful to screen
CC   for homologous nucleic acids which are required for cell proliferation in
CC   a wide variety of organisms. The present sequence is an antisense
CC   oligonucleotide of the invention.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 298 BP; 91 A; 69 C; 43 G; 95 T; 0 other;
```

```
  Query Match           60.5%;  Score 234;  DB 23;  Length 298;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-56;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 124

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 184

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 244

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCA 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCA 298
```

RESULT 11
AAS50723
ID AAS50723 standard; DNA; 298 BP.
XX
AC AAS50723;
XX
DT 13-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation inhibitory sequence #1947.
XX
KW Antisense; ss; prokaryotic cellular proliferation;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 1; Seq ID No 3300; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence is an antisense
CC oligonucleotide of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 298 BP; 91 A; 69 C; 43 G; 95 T; 0 other;

```
  Query Match           60.5%;  Score 234;  DB 23;  Length 298;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-56;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 124

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 184

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 244

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCA 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCA 298
```

RESULT 12
ABQ67194/c
ID ABQ67194 standard; DNA; 319630 BP.
XX
AC ABQ67194;
XX
DT 29-AUG-2002 (first entry)
XX
DE Listeria innocua contig DNA sequence #7.
XX
KW Antibacterial; Listeria; food contamination; mutational analysis;
KW infection; ds.
XX
OS Listeria innocua.
XX
PN WO200228891-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-FR03061.
XX
PR 04-OCT-2000; 2000FR-0012697.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Kunst F, Glaser P;
XX
DR WPI; 2002-332479/37.
XX
PT New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX
PS Claim 5; SEQ ID 7; 180pp; French.
XX
CC The present invention relates to nucleic acid sequences
CC (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be

```
CC   used to screen for compounds that modulate gene expression, replication
CC   and pathogenicity of Listeria (potential therapeutic agents), also for
CC   treating infections by Listeria, and are useful as immunogens in
CC   anti-Listeria vaccines.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 319630 BP; 105207 A; 55428 C; 66726 G; 92263 T; 6 other;

  Query Match             53.2%;  Score 205.8;  DB 24;  Length 319630;
  Best Local Similarity   70.9%;  Pred. No. 5.5e-47;
  Matches  273;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| ||||    |||||||| |  ||| ||||| | ||  |||||||| ||||
Db      51123 TCCTCTTCTTCTTTTGGAAAATGAGCACGAACAGCATCAAGCATATCACCAAGCCCTAGT 51064

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              ||||| || || || || |||||||| |||||||| || |  ||||| || ||||| |
Db      51063 CCATGAGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATC 51004

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              |    |||||||||    |||||||||| |||| |||||| || |  ||||| |||||
Db      51003 TGATCACGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 50944

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
              ||| | |||||  || ||   ||| ||    |  || |  |||||||  | ||
Db      50943 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACCCCTTCACGACCATTGGTA 50884

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||||||  || || |||||||  || ||||||||  || || || | ||||||   |
Db      50883 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 50824

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              |||||||  | ||    ||  ||||||||||||||||||||||| || || || | |
Db      50823 AAGAATGGTTCGTCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 50764

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              | ||||||  |||||  ||| || |
Db      50763 AGCCATTCCGCTGAATTATATATGC 50739


RESULT 13
ABA03041
ID   ABA03041 standard; DNA; 2944528 BP.
XX
AC   ABA03041;
XX
DT   05-FEB-2002  (first entry)
XX
DE   Listeria monocytogenes EGD-e genome sequence.
XX
KW   Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW   vitamin B12; bacterial infection; disease; ds.
XX
OS   Listeria monocytogenes.
XX
PN   WO200177335-A2.
XX
PD   18-OCT-2001.
XX
PF   11-APR-2001; 2001WO-FR01118.
XX
PR   11-APR-2000; 2000FR-0004629.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Buchrieser C,  Frangeul L,  Couve E,  Rusniok C,  Fsihi H,  Dehoux P;
PI   Dussurget O,  Chetouani F,  Nedjari H,  Glaser P,  Kunst F,  Cossart P;
PI   Daniels J,  Goebel W,  Kreft J,  Kuhn M,  Ng E,  Vazquez-Boland JA;
PI   Dominguez-Bernal G,  Garrido-Garcia P,  Tierrez-Martinez A,  Amend A;
PI   Chakraborty T,  Domann E,  Hain T,  Berche P,  Charbit A,  Durant L;
PI   Perez-Diaz J,  Baquero F,  Garcia Del Portillo F,  Gomez-Lopez N;
PI   Maduenio E,  De Pablos B,  Wehland J,  Kaerst U,  Entian K,  Hauf J;
PI   Rose M,  Voss H;
XX
DR   WPI; 2002-010914/01.
XX
PT   Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT   and prevention of Listeria and related bacterial infections, and
PT   related polypeptides  -
XX
PS   Claim 1; SEQ ID No 1; 192pp; French.
XX
CC   The present sequence is the genome sequence of Listeria monocytogenes
CC   EGD-e. This sequence and fragments of this sequence are useful for
CC   selecting probes and primers for detecting genes in L. monocytogenes and
CC   related organisms, and to study genetic polymorphisms and other genomes.
CC   Proteins (ABB47297-ABB50149) expressed from the present sequence are
CC   useful for raising specific antibodies, identification of L.
CC   monocytogenes and related organisms, and for biosynthesis and
CC   biodegradation, especially biosynthesis of Vitamin B12. This sequence and
CC   proteins encoded by it are also useful for selecting compounds that
CC   regulate gene expression and cell replication and modulate L.
CC   monocytogenes-related diseases. In addition, this sequence and proteins
CC   encoded by it are useful in pharmaceutical and vaccines compositions for
CC   the treatment or prevention of infections by L. monocytogenes and related
CC   organisms.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;

  Query Match             53.2%;  Score 205.8;  DB 24;  Length 2944528;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-46;
  Matches  273;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| ||||    |||||||| |  ||| ||||| | ||  |||||||| ||||
Db    2011933 TCCTCTTCTTCTTTTGGAAAATGAGCGCGAACAGCATCAAGCATGTCGCCAAGCCCTAGT 2011992

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              |||||||| || || || |||||||| |||||||| || |  ||||| || ||||| |
Db    2011993 CCATGTGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATT 2012052

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              |    ||||||||    |||||||||| |||| |||||| || |  ||||| |||||
Db    2012053 TGATCTCGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 2012112

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
              ||| | |||||  || ||   ||| ||    |  || |  |||||||  | ||
Db    2012113 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACTCCTTCACGACCATTGGTA 2012172

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||||||  || || |||||||  || ||||||||  || || || | ||||||   |
Db    2012173 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 2012232

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              |||||| ||||   ||  |||||||||||||||||||||| || || || | |
Db    2012233 AAAAATGGTTCATCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 2012292

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              | ||||||  |||||  ||| || |
Db    2012293 AGCCATTCCGCTGAATTATATATGC 2012317


RESULT 14
ABQ69245
ID   ABQ69245 standard; DNA; 3011208 BP.
XX
AC   ABQ69245;
XX
DT   29-AUG-2002  (first entry)
XX
```

```
DE   Listeria innocua DNA sequence #684.
XX
KW   Antibacterial; Listeria; food contamination; mutational analysis;
KW   infection; ds.
XX
OS   Listeria innocua.
XX
PN   WO200228891-A2.
XX
PD   11-APR-2002.
XX
PF   04-OCT-2001; 2001WO-FR03061.
XX
PR   04-OCT-2000; 2000FR-0012697.
XX
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Kunst F,  Glaser P;
XX
DR   WPI; 2002-332479/37.
XX
PT   New genomic sequences from Listeria species, useful for detection,
PT   treatment and prevention of infection, also related polypeptides,
PT   antibodies and modulators -
XX
PS   Claim 5; SEQ ID 2058; 180pp; French.
XX
CC   The present invention relates to nucleic acid sequences
CC   (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes
CC   and primers for identification and/or detection of Listeria (e.g. as
CC   contaminants in foods, or mutational analysis) and for analysis of
CC   gene expression. Proteins encoded by the nucleic acid sequences can be
CC   used to screen for compounds that modulate gene expression, replication
CC   and pathogenicity of Listeria (potential therapeutic agents), also for
CC   treating infections by Listeria, and are useful as immunogens in
CC   anti-Listeria vaccines.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3011208 BP; 941651 A; 568176 C; 559189 G; 942192 T; 0 other;

  Query Match             53.2%;  Score 205.8;  DB 24;  Length 3011208;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-46;
  Matches  273;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| |||| |||||||| | ||| ||||| | ||  |||||||| ||||
Db    2066305 TCCTCTTCTTCTTTTGGAAAATGAGCACGAACAGCATCAAGCATATCACCAAGCCCTAGT 2066364

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              ||||| || || || || |||||||| |||||||| || |  ||||| || ||||| |
Db    2066365 CCATGAGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATC 2066424

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              |    |||||||||    |||||||||| |||| |||||| || |  ||||| |||||
Db    2066425 TGATCACGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 2066484

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
              ||| | |||||  || ||  ||| ||    |  || |  |||||||  | ||
Db    2066485 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACCCCTTCACGACCATTGGTA 2066544

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||||||| || || |||||||| || |||||||| || || || | ||||||   |
Db    2066545 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 2066604

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              ||||||| | ||   ||  |||||||||||||||||||||| || || || | |
Db    2066605 AAGAATGGTTCGTCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 2066664

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              | ||||||  |||||  ||| || |
```

```
Db    2066665 AGCCATTCCGCTGAATTATATATGC 2066689


RESULT 15
ABK75008/c
ID   ABK75008 standard; DNA; 1311 BP.
XX
AC   ABK75008;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Bacillus licheniformis genomic sequence tag (GST) #2299.
XX
KW   Differential gene expression; genomic sequenced tag; GST;
KW   altered culture condition; environmental stress;
KW   physiological provocation; ds.
XX
OS   Bacillus licheniformis.
XX
PN   WO200229113-A2.
XX
PD   11-APR-2002.
XX
PF   05-OCT-2001; 2001WO-US31437.
XX
PR   06-OCT-2000; 2000US-0680598.
PR   27-MAR-2001; 2001US-279526P.
XX
PA   (NOVO ) NOVOZYMES BIOTECH INC.
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Berka R,  Clausen IG;
XX
DR   WPI; 2002-416684/44.
XX
PT   Monitoring differential expression of several genes in first Bacillus
PT   cell relative to expression of same genes in one or more second
PT   Bacillus cells, by using substrate containing Bacillus genomic
PT   sequenced tag array -
XX
PS   Claim 4; SEQ ID NO 2299; 200pp; English.
XX
CC   The invention describes a method of monitoring differential expression of
CC   genes in a first Bacillus cell relative to expression of the genes in
CC   other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC   isolated from Bacillus cells to a substrate containing array of Bacillus
CC   genomic sequenced tags (GST), examining the array, and determining
CC   relative gene expression by an observed hybridisation reporter signal of
CC   a spot in the array. The method is useful for measuring the expression of
CC   genes in a first Bacillus cell relative to expression of the same genes
CC   in one or more second Bacillus cells. The method is useful for monitoring
CC   global expression of several genes from a Bacillus cell, discovering new
CC   genes, identifying possible functions of unknown open reading frames and
CC   monitoring gene copy number variation and stability. Monitoring changes
CC   in expression of genes may be used to provide a representation of the way
CC   in which Bacillus cells adapt to changes in culture conditions,
CC   environmental stress or other physiological provocation. Extensive
CC   follow-up characterisation is unnecessary, when one spot on an array
CC   equals one gene or one open reading frame, since sequence information is
CC   available. This sequence represents a genomic sequence tag (GST) used in
CC   the method of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1311 BP; 376 A; 279 C; 353 G; 303 T; 0 other;

  Query Match             45.1%;  Score 174.4;  DB 24;  Length 1311;
  Best Local Similarity   67.1%;  Pred. No. 6.1e-39;
  Matches  247;  Conservative    0;  Mismatches  121;  Indels    0;  Gaps    0;

Qy         20 AAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAACCATGTGACCCTGATAT 79
```

```
Db        489 AAAATGTTCGCTGACCGCGTCAAGCAGATCGCCGAGACCAAGGCCATGCGTCCATGAAAT 430

Qy         80 CGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACGTCTGTACGCATTTCCAT 139

Db        429 CGGGAACGGCTCGCCAAAGCCGAGGGCATAAAAATCGTAAATGTTTGCTCTCATTTCAGG 370

Qy        140 ATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGATTTGTATAAAATTTGAGC 199

Db        369 ATTATCCACTTTATTAACCGCCAGAACGACGGGTTTTTTTGTACGGTATAAAATTTTCGC 310

Qy        200 GACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACCATAAAAATAATAACATC 259

Db        309 CACTTCTTCATCAGCGGCTGTGACGCCTTCGCGGCCGTTCGTCATGAAAATAATCACATC 250

Qy        260 CGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTTTGGAATGGTGCATCACC 319

Db        249 TGCTTCTTCCATGGCGATCTCGGCCTGATGGCGAATCTGCGCCAAAAACGGCTCATCGCC 190

Qy        320 AATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTTAACCATTCACCTGAAGA 379

Db        189 GACTTCGATTCCGCCTGTATCAATCAGGTTGAAGTCGTGATTCAGCCACTCGGCAGAGCT 130

Qy        380 ATAAATAC 387

Db        129 GTATATCC 122

Search completed: September 12, 2003, 17:32:09
Job time : 138.915 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 12, 2003, 17:17:09 ; Search time 1580.02 Seconds
(without alignments)
10020.134 Million cell updates/sec

Title: US-09-815-242-1463
Perfect score: 387
Sequence: 1 gatcttcttcctcttcacca.....ttcacctgaagaataaatac 387

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	387	100.0	1308	6	AX622668	AX622668 Sequence
2	387	100.0	301550	1	AP003134	AP003134 Staphyloc
3	387	100.0	333750	1	AP004827	AP004827 Staphyloc
4	387	100.0	345900	1	AP003362	AP003362 Staphyloc
5	262.2	67.8	3269	1	AF270032	AF270032 Staphyloc
6	262.2	67.8	3269	6	AX145350	AX145350 Sequence
7	262.2	67.8	300892	1	AE016747	AE016747 Staphyloc
c 8	210.6	54.4	290117	1	AE017028	AE017028 Bacillus
c 9	209	54.0	304680	1	AE017002	AE017002 Bacillus
10	205.8	53.2	313450	1	AL596170	AL596170 Listeria
c 11	205.8	53.2	319630	6	AX413016	AX413016 Sequence
12	205.8	53.2	347050	1	AL591981	AL591981 Listeria
13	205.8	53.2	349980	6	AX417046	AX417046 Sequence
14	205.8	53.2	349980	6	AX641670	AX641670 Sequence
c 15	198.4	51.3	24887	1	BACSERA	L47648 Bacillus su
16	198.4	51.3	213680	1	BSUB0012	Z99115 Bacillus su
c 17	191.4	49.5	302173	1	AE016951	AE016951 Enterococ
18	188.2	48.6	300050	1	AP004599	AP004599 Oceanobac
c 19	185	47.8	300550	1	AP001512	AP001512 Bacillus
20	182.4	47.1	302050	1	AL935257	AL935257 Lactobaci
c 21	174.4	45.1	1311	6	AX433884	AX433884 Sequence
c 22	162.6	42.0	11071	1	AE006309	AE006309 Lactococc
c 23	162.6	42.0	12434	1	AE006498	AE006498 Streptoco
c 24	162	41.9	1311	6	AX607165	AX607165 Sequence
25	162	41.9	44145	6	AX602195	AX602195 Sequence
26	162	41.9	174050	1	SAG766852	AL766852 Streptoco
27	160.4	41.4	20601	1	AE014265	AE014265 Streptoco
c 28	159.4	41.2	52276	1	AE014141	AE014141 Streptoco
29	159.4	41.2	323825	1	AP005146	AP005146 Streptoco
c 30	157.8	40.8	12370	1	AE009978	AE009978 Streptoco
31	153	39.5	12540	1	AE008523	AE008523 Streptoco
c 32	151.4	39.1	1308	6	AX570314	AX570314 Sequence
33	151.4	39.1	5066	6	AR218847	AR218847 Sequence
34	151.4	39.1	5066	6	BD003759	BD003759 Polynucle
35	151.4	39.1	10310	1	AE007464	AE007464 Streptoco
36	151.4	39.1	151947	2	SPNEU1902	AL449924 Streptoco
37	151.4	39.1	349980	6	AX571764	AX571764 Sequence
38	151.4	39.1	349980	6	AX571765	AX571765 Sequence
39	149.8	38.7	13860	1	AE015016	AE015016 Streptoco
c 40	148.2	38.3	3737	1	AB016077	AB016077 Streptoco
c 41	139.4	36.0	301278	1	AE015939	AE015939 Clostridi
42	125.2	32.4	296750	1	AP003191	AP003191 Clostridi
c 43	117	30.2	10861	1	AE007680	AE007680 Clostridi
c 44	109.2	28.2	3557	1	AY094626	AY094626 Lactobaci
c 45	101	26.1	960	6	AX144037	AX144037 Sequence

ALIGNMENTS

RESULT 1
AX622668/c
LOCUS AX622668 1308 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 5631 from Patent WO02094868.
ACCESSION AX622668
VERSION AX622668.1 GI:28450653
KEYWORDS .
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1
AUTHORS Masignani,V.C., Mora,M.C. and Scarselli,M.C.
TITLE Staphylococcus aureus proteins and nucleic acids
JOURNAL Patent: WO 02094868-A 5631 28-NOV-2002;
Chiron Spa (IT)

```
FEATURES             Location/Qualifiers
     source          1. .1308
                     /organism="Staphylococcus aureus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1280"
BASE COUNT      450 a    184 c    278 g    396 t
ORIGIN

  Query Match           100.0%;  Score 387;  DB 6;  Length 1308;
  Best Local Similarity  100.0%;  Pred. No. 2e-77;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 449

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 389

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 329

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 269

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 209

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 149

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||||||||||||||||||||||
Db        148 TTAACCATTCACCTGAAGAATAAATAC 122


RESULT 2
AP003134
LOCUS       AP003134               301550 bp    DNA     linear   BCT 24-APR-2003
DEFINITION  Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
            genome, section 6/10.
ACCESSION   AP003134 BA000018
VERSION     AP003134.2  GI:14349226
KEYWORDS    .
SOURCE      Staphylococcus aureus subsp. aureus N315
  ORGANISM  Staphylococcus aureus subsp. aureus N315
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1
  AUTHORS   Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
            Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
            Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
            Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
            Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
            Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
            Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
  TITLE     Whole genome sequencing of meticillin-resistant Staphylococcus
            aureus
  JOURNAL   Lancet 357 (9264), 1225-1240 (2001)
  MEDLINE   21311952
   PUBMED   11418146
REFERENCE   2  (bases 1 to 301550)
  AUTHORS   Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
            Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-2001) Director-General, Biotechnology Center,
            National Institute of Technology and Evaluation, Biotechnology
            Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
            (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
            Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT     On Jun 12, 2001 this sequence version replaced gi:13701258.
FEATURES             Location/Qualifiers
     source          1. .301550
                     /organism="Staphylococcus aureus subsp. aureus N315"
                     /mol_type="genomic DNA"
                     /strain="N315"
                     /sub_species="aureus N315"
                     /db_xref="taxon:158879"
     gene            complement(249. .947)
                     /gene="SA1293"
     CDS             complement(249. .947)
                     /gene="SA1293"
                     /note="ORFID:SA1293"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="BAB42553.1"
                     /db_xref="GI:13701259"
                     /translation="MSSIFTMIIYFVILMVLPLWAQHKVKSNYEKYSQVRSTSGKTGR
                     EVALEILHANGIYDVEVVKGEGFLTDHYDPKKKVVSLSPANYDRPSVAGTAIAAHEVG
                     HAIQDHQGYWFLRFRAALVPVANLGSSLSYMIIMLGIILTAIGSAFGSTALWIGAGLM
                     SLAVLFSIVTLPVEFDASSRAMKQITALNIVNEKEYKHARKVLSAAAMTYVAATAVAV
                     AELVRIILIARSSD"
     gene            complement(1001. .1588)
                     /gene="SA1294"
     CDS             complement(1001. .1588)
                     /gene="SA1294"
                     /note="ORFID:SA1294"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="BAB42554.1"
                     /db_xref="GI:13701260"
                     /translation="MTINTFWQYTLYQRSWLMMLLICNILGMIYGYIWYGEQLSHTPW
                     HFKIFVPDSPTAILYLVISISLILIQKQNSIIEALAFVTLFKYGIWAVIMNILFIIEQ
                     GDITVNGLVLMFSHSIMAVQAIYFYPRFKRSMIGISVAMIWVFLNDYIDYFHLQFPYY
                     DFITTHVWQIGVLSCCLSVFGLLLYIELNKLLKCK"
     gene            complement(1578. .2153)
                     /gene="SA1295"
     CDS             complement(1578. .2153)
                     /gene="SA1295"
                     /note="ORFID:SA1295"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="BAB42555.1"
                     /db_xref="GI:13701261"
                     /translation="MSETLNQIKESFIEYLLFQYRFKSRIAVWVLNYIKVNEAKLANI
                     HFVDTKINHHETLEIAEVGSHASAIQFTKRNIKLMNTNEIFDYIANHNCAFDIQIHFA
                     NVSKREQRLDDLIVAQLTESPSYQTYLHDLNSMAIDRHKHALLIDYLLHNIDLSLQMN
                     EKQRFYQLTQILNTLKLVNKHNQFEDLADDD"
     gene            complement(2167. .3411)
                     /gene="SA1296"
     CDS             complement(2167. .3411)
                     /gene="SA1296"
                     /note="ORFID:SA1296"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="BAB42556.1"
                     /db_xref="GI:13701262"
                     /translation="MEDIYKLIDDINLQKLENLDSRVNEAITTDNDDALFILGETLYN
                     FGLMPQGLEVFRVLYHKYPDESELLIYFIEGLMSENQTDEALEYLSYVEPSPEKLMLE
                     ADLYQQINMMEVAIDKLQEALELEPNDPIIHFALAEMLYYDGQYLRATSEYETVLETG
                     EYQVNGVNLFSRMADCSLQSGNYSDAIRLYDEINEDEMTSEDYLKKAISYDKNDITQE
                     AIKIMTTLLSKDPDYIQGYLYLQSLYENEKNYPDAIETGKEGLRLSQFYKELMYTTGC
                     LEIEHGDANEGVLLLKQALEVDNAYQEPLLILSDLYRNEEDYEAIIELLTYVDEEDLD
                     PTFMWHLAFAYGQEERDKEAQHFFELAYPTMKTNIDFMSDYYFYLIEIGQKEQAITIL
                     NQLLELEPSNENWHDELSRLQS"
     gene            complement(3418. .4716)
                     /gene="aroA"
     CDS             complement(3418. .4716)
```

```
                /gene="aroA"
                /note="ORFID:SA1297"
                /codon_start=1
                /transl_table=11
                /product="3-phosphoshikimate 1-carboxyvinyltransferase"
                /protein_id="BAB42557.1"
                /db_xref="GI:13701263"
                /translation="MVSEQIIDISGPLKGEIEVPGDKSMTHRAIMLASLAEGTSNIYK
                PLLGEDCRRTMDIFRLLGVDIKEDEDKLVVNSPGYKAFKTPHQVLYTGNSGTTTRLLA
                GLLSGLGIESVLSGDVSIGKRPMDRVLRPLKLMDANIEGIEDNYTPLIIKPSVIKGIN
                YQMEVASAQVKSAILFASLFSNDTTVIKELDVSRNHTETMFRHFNIPIEAERLSITTT
                PDAIQHIKPADFHVPGDISSAAFFIVAALITPESDVTIHNVGINPTRSGIIDIVEKMG
                GNIQLFNQTTGAEPTASIRIQYTPMLQPITIEGELVPKAIDELPVIALLCTQAVGTST
                IKDAEELKVKETNRIDTTADMLNLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIG
                MMLAVASLLSSEPVKIKQFDAVNVSFPGFLPKLKLLENEG"
gene            complement(4726. .5790)
                /gene="aroB"
CDS             complement(4726. .5790)
                /gene="aroB"
                /note="ORFID:SA1298"
                /codon_start=1
                /transl_table=11
                /product="3-dehydroquinate synthase"
                /protein_id="BAB42558.1"
                /db_xref="GI:13701264"
                /translation="MKLQTTYPSNNYPIFVEHGAIDHISTYIDQFDQSFILIDEHVNQ
                YFADKFDDILSYENVHKVIIPAGEKTKTFEQYQETLEYILSHHVTRNTAIIAVGGGAT
                GDFAGFVAATLLRGVHFIQVPTTILAHDSSVGGKVGINSKQGKNLIGAFYRPTAVIYD
                LDFLKTLPFEQILSGYAEVYKHALLNGESTTQEIEQHFKDREILQSLNGMDKYIAKGI
                ETKLDIVVADEKEQGVRKFLNLGHTFGHAVEYNHKIAHGHAVMIGIIYQFIVANILFN
                SNHDIQHYINYLTKLGYPLETITDIDFETIYQYMLSDKKNDKQGVQMVLIKHFGDIVV
                QHIDQTTLQHACEQLKTYFK"
gene            complement(5816. .6982)
                /gene="aroC"
CDS             complement(5816. .6982)
                /gene="aroC"
                /note="ORFID:SA1299"
                /codon_start=1
                /transl_table=11
                /product="chorismate synthase"
                /protein_id="BAB42559.1"
                /db_xref="GI:13701265"
                /translation="MRYLTSGESHGPQLTVIVEGIPANLEIKVEDINKEMFKRQGGYG
                RGRRMQIEKDTVEIVSGVRNGYTLGSPITMVVTNDDFTHWRKIMGAAPISEEERENMK
                RTITKPRPGHADLVGGMKYNHRDLRNVLERSSARETAARVAVGALCKVLLQQLDIDIY
                SRVVEIGGIKDKDFYDSETFKANLDRNDVRVIDDSIAQAMRDKIDEAKNEGDSIGGVV
                QVVVENMPVGVGSYVHYDRKLDGKIAQGVVSINAFKGVSFGEGFKAAEKPGSEIQDEI
                LYNSEIGYYRGSNHLGGLEGGMSNGMPIIVNGVMKPIPTLYKPLNSVDINTKEDFKAT
                IERSDSCAVPAASIVCEHVVAFEIAKALLEEFQSNHIEQLQQQIADRRQLNVEF"
gene            complement(7368. .7568)
                /gene="SA1300"
CDS             complement(7368. .7568)
                /gene="SA1300"
                /note="ORFID:SA1300"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein"
                /protein_id="BAB42560.1"
                /db_xref="GI:13701266"
                /translation="MKNIISIILGILMFLKLMELLYGAIFLDKPLNPITKIIFILTLI
                YIFYVLVKELIIFLKSKYNKSA"
gene            complement(7597. .7722)
                /gene="SAS045"
CDS             complement(7597. .7722)
                /gene="SAS045"
                /note="ORFID:SAS045"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein"
                /protein_id="BAB42561.1"
                /db_xref="GI:13701267"
                /translation="MWLVIMIIHNKARFLCCSKLLEKFYSFLVTRIKKRGIFFIK"
gene            complement(7777. .8226)
                /gene="ndk"
CDS             complement(7777. .8226)
                /gene="ndk"
                /note="ORFID:SA1301"
                /codon_start=1
                /transl_table=11
                /product="nucleoside diphosphate kinase"
                /protein_id="BAB42562.1"
                /db_xref="GI:13701268"
                /translation="MERTFLMIKPDAVQRNLIGEVISRIERKGLKLVGGKLMQVPMEL
                AETHYGEHQGKPFYNDLISFITSAPVFAMVVEGEDAVNVSRHIIGSTNPSEASPGSIR
                GDLGLTVGRNIIHGSDSLESAEREINLWFNENEITSYASPRDAWLYE"
gene            complement(8318. .9277)
                /gene="gerCC"
CDS             complement(8318. .9277)
                /gene="gerCC"
                /note="ORFID:SA1302"
                /codon_start=1
                /transl_table=11
                /product="heptaprenyl diphosphate syntase component II"
                /protein_id="BAB42563.1"
                /db_xref="GI:13701269"
                /translation="MAKLNMNNEIKKVEQRLEKAIKSKDSVLEQASLHLLSSGGKRVR
                PAFVILSSQFGKDEQTSEQTYQVAVALELIHMATLVHDDVIDKSDKRRGKLTISKKWD
```

```
 Query Match             100.0%;  Score 387;  DB 1;  Length 301550;
 Best Local Similarity   100.0%;  Pred. No. 1.2e-77;
 Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13271 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 13330

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13331 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 13390

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13391 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 13450

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13451 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 13510

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13511 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 13570

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13571 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 13630

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              |||||||||||||||||||||||||||
Db      13631 TTAACCATTCACCTGAAGAATAAATAC 13657
```

```
RESULT 3
AP004827
LOCUS       AP004827              333750 bp    DNA     linear   BCT 24-APR-2003
DEFINITION  Staphylococcus aureus subsp. aureus MW2 DNA, complete genome,
            strain:MW2, section 6/10.
ACCESSION   AP004827 BA000033
VERSION     AP004827.1  GI:21204509
KEYWORDS    .
SOURCE      Staphylococcus aureus subsp. aureus MW2
  ORGANISM  Staphylococcus aureus subsp. aureus MW2
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1
  AUTHORS   Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A.,
            Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L.,
            Yamamoto,K. and Hiramatsu,K.
```

```
  TITLE     Genome and virulence determinants of high virulence
            community-acquired MRSA
  JOURNAL   Lancet 359 (9320), 1819-1827 (2002)
  MEDLINE   22040717
   PUBMED   12044378
REFERENCE   2  (bases 1 to 333750)
  AUTHORS   Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
            Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
            Kikuchi,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAR-2002) Director-General, Biotechnology Center,
            National Institute of Technology and Evaluation, Biotechnology
            Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
            (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
            Tel:81-3-3481-1933, Fax:81-3-3481-8424)
FEATURES             Location/Qualifiers
     source          1. .333750
                     /organism="Staphylococcus aureus subsp. aureus MW2"
                     /mol_type="genomic DNA"
                     /strain="MW2"
                     /db_xref="taxon:196620"
     gene            complement(278. .619)
                     /gene="MW1341"
     CDS             complement(278. .619)
                     /gene="MW1341"
                     /note="ORFID:MW1341"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB95206.1"
                     /db_xref="GI:21204510"
                     /translation="MTNITKEVFDNLEQEIDVFAKNKTLGSSEAKPYLDEYHSKIIDY
                     FKQVNDITGNIDFDKLNQYPVVPMNFKERYDYMIERKYHFMGYRQMKTFKTELIKMNA
                     SYQTRLKNKQV"
     gene            complement(624. .1283)
                     /gene="nth"
     CDS             complement(624. .1283)
                     /gene="nth"
                     /note="ORFID:MW1342"
                     /codon_start=1
                     /transl_table=11
                     /product="endonuclease-like protein"
                     /protein_id="BAB95207.1"
                     /db_xref="GI:21204511"
                     /translation="MVSKKKALEMIDVIANNFPDAECELKHDNPFELTIAVLLSAQCT
                     DVLVNRVTTELFKKYKTPEDYLAVSDEELMNDIRSIGLYRNKAKNIKKLCQSLIDQFN
                     GEIPQTHKELESLAGVGRKTANVVMSVAFDEPSLAVDTHVERVSKRLGINRWKDNVRQ
                     VEDRLCSVIPRDRWNRSHHQLIFFGRYHCLARKPKCDICPLLEDCREGQKRYKASLKE
                     A"
     gene            complement(1273. .1959)
                     /gene="MW1343"
     CDS             complement(1273. .1959)
                     /gene="MW1343"
                     /note="ORFID:MW1343
                     hypothetical protein, similar to chromosome replication
                     initiation protein dnaD"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="BAB95208.1"
                     /db_xref="GI:21204512"
                     /translation="MDKYQLKARPVVIRRELLDHYSDLGLDEQDLVILLKLIYASETS
                     NKQPSIELLQKGSTMQPRDITMVIQNLIQRELLELQVQKDEEGRFTEYMNLDPFFEKL
                     SHILKQQSMETKEQNSKEKFKQLFRVLEDTFARPLSPYEIETLNQWIDVDKHDSAIIQ
                     AALDEANSLNKLSFKYMDRILLNWKKNNVKTIDDSRKIREKFNKPKMTHTVKTVPKFD
                     WLNGENLDGK"
     gene            complement(2287. .3579)
                     /gene="asnS"
     CDS             complement(2287. .3579)
                     /gene="asnS"
                     /note="ORFID:MW1344"
                     /codon_start=1
                     /transl_table=11
                     /product="asparaginyl-tRNA synthetase"
                     /protein_id="BAB95209.1"
                     /db_xref="GI:21204513"
                     /translation="MKTTIKQAKDKLNQDVTIGAWLTNKRSSGKIAFLQLRDGTGFMQ
                     GVVVKSEVDEEVFKLAKEITQESSLYVTGTITEDNRSDLGYEMQVKSIEVISEAHDYP
                     ITPKNHGTEFLMDHRHLWLRSKKQHAVMKIRNEVIRATYEFFNKDGFTKVDPPILTAS
                     APEGTSELFHTKYFDQDAFLSQSGQLYLEAAAMAHGKVFSFGPTFRAEKSKTRRHLIE
                     FWMIEGEMAFTNHAESLEIQEQYVTHVVKSVLENCKLELKILERDTSKLEKVATPFPR
                     ISYDDAIEFLKSEGFDDIEWGEDFGAPHETAIANHYDLPVFITNYPTKIKPFYMQPNP
                     ENEETVLCADLIAPEGYGEIIGGSERVDDLELLEQRVKEHGLDEEAYSYYLDLRRYGS
                     VPHCGFGLGLERTVAWISGVEHVRETAPFPRLLNRLYP"
     gene            complement(3901. .6594)
                     /gene="dinG"
     CDS             complement(3901. .6594)
                     /gene="dinG"
                     /note="ORFID:MW1345"
                     /codon_start=1
                     /transl_table=11
                     /product="probable ATP-dependent DNA helicase dinG"
                     /protein_id="BAB95210.1"
                     /db_xref="GI:21204514"
                     /translation="MGMATYAVVDLETTGNQLDFDDIIQIGITFVRNNQIIDTYHSMI
                     RTNLEIPPFIQALTSIEENMLQQAPYFNQVAQEIYDKIKDCIFVAHNVDFDLNFIKKA
                     FKDCNIQYRPKKVIDTLEIFKIAFPTDKSYQLSELAEAHGITLANAHRADEDAATTAK
                     LMILAFEKFEKLPLDTLKQLYYLSKQLKYDLYDIFFEMVRQYDAKPLDKSYEKFEQII
                     YRKQVDFKKPTTNYNGSLKSLYSKAVDQLGL7YRPQQLYLAETILDQLMHSEKAMIEA
                     SLGSGKSLAYLLAALMYNIETGKHVMISTNTKLLQSQLLEKDIPAMNEALNFKINALL
                     IKSKSDYISLGLISQILKDDTSNYEVNILKMQLLIWITETPSGDIQELNLKGGQKMYF
                     DQKIETYVPARHDVHYYNFIKRNAQNIQIGITNHAHLIHSDVENSIYQLFDDCIVDEA
                     HRLPDYALNQVTNELSYADIKYQLGLIGKNENEKLLKAIDQLEKQRILEKLDIAPIDI
                     FGLKASMNEIHELNEQLFSTIFTIINDSDVYDDDIHRFHNVFTFETKDILKDLHAIID
                     KLNKTLEIFNGISHKTVKSLRKQLLYLKDKFKNIEQSLKAGHTSFISIKNLSQKSTIR
                     LYVKDYAVKDVLTKQVLEKFKSLIFISGTLKFNHSFEAFKQLFNKDVHFNTFEVNTSL
                     QSAKNTSVFIPSDVASYQYKNIDEYVASIVSYIIEYTTITSSKCLVLFTSYKMMHMVQ
                     DMLNELPEFEDYVVLTQQQNQNYKIVQQFNNFDKAILLGTSTFFEGFDFQANGIKCVM
                     IAKLPFMNKHNAKYWLMDSEFTSTFKEYVLPDAVTRFRQGLGRLIRSENDRGIIVSFD
                     DRLINSNYKNFFEQTLENYRQKKGDIQQFGKLLRQIQKKKK"
     gene            complement(6618. .7589)
                     /gene="MW1346"
     CDS             complement(6618. .7589)
                     /gene="MW1346"
                     /note="ORFID:MW1346"
                     /codon_start=1
                     /transl_table=11
                     /product="truncated hypothetical protein"
                     /protein_id="BAB95211.1"
                     /db_xref="GI:21204515"
                     /translation="MSKYSQDVLQLLYKNKPNYISGQSIAESLNISRTAVKKVIDQLK
                     LEGCKIDSVNHKGHLLQQLPDIWYQGIIDQYTKSSALFDFSEVYDSIDSTQLAAKKSL
                     VGNQSSFFILSDEQTKGRGRFNRHWSSSKGQGLWMSVVLRPNVAFSMISKFNLFIALG
                     IRDAIQHFSQDEVKVKWPNDIYIDNGKVCGFLTEMVANNDGIEAIICGIGINLTQQLE
                     NFDESIRHRATSVQLHDKNKLDRYQFLERLLQEIEKRYNQFLTLPFSEIREEYIAASN
                     IWNRTLLFTENDKQFKGQAIDLDYDGYLIVRDEAGESHRLISADIDF"
     gene            complement(7576. .8778)
                     /gene="MW1347"
     CDS             complement(7576. .8778)
                     /gene="MW1347"
                     /note="ORFID:MW1347
                     hypothetical protein, similar to poly(A) polymerase"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="BAB95212.1"
                     /db_xref="GI:21204516"
                     /translation="MDKSLFEQARPILEQIQDNGFEAYYVGGSVRDYVMGRNIHDIDI
                     TTSATPDEIESIFSHTIPVGKEHGTINVVFNDENYEVTTFRAEEDYVDHRRPSGVTFV
                     RDLYEDLQRRDFTMNAIAMDTAYKLYDYFDGQQDINNRIIRTVGIAEERFQEDALRMI
                     RCLRFQSQLSFDIATETFEAMRIQMADIKFLSIERIVIELTKLMRGINVEKSFNHLKS
                     LKAFNYMPYFEHLDMNQINVTEAIDLELLIAIVSVKFDINYSLKPLKLSNRQVKDINQ
                     YIQIMNALPSIITKEQLKMFVYDYDTHLIKNVMVAADVIKANDIQGHEPLIVNLQTID
                     ETLHRLPMHNRKDMMVNGGVLMAHLNAKSGPWLKDVLRQIEIAIVTGKVSNEETEILK
                     WVDNHVKI"
     gene            complement(8783. .9925)
                     /gene="MW1348"
     CDS             complement(8783. .9925)
```

```
                     /gene="MW1348"
                     /note="ORFID:MW1348
                     hypothetical protein, similar to lipopolysaccharide
                     biosynthesis-related pr homolog"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="BAB95213.1"
                     /db_xref="GI:21204517"
                     /translation="MKIGITCYPSMGGSGIIATELGIKLAERGHEVHFITSNIPFRIR
                     KPLPNMIFHQVEVNQYAVFQYPPYDITLSTKIAEVIKEYGLDLLHMHYAVPHAICGIL
                     AREMSGKDIKIMTTLHGTDITVLGYDHSLQGAIKFGIEKSDIVTSVSKSLAQETHEII
                     ETNKEIIPIYNFVRENEFPTKHNTALKSQFGIAPDEKVLIHVSNFRQVKRIDTIIETF
                     AKVREKIPSKLILLGDGPELVPMRQLTKELNVEEDVLFLGKQDCVSEFYQLSDLVLLL
                     SEKESFGLTLLEAMKTGVVPIGSNAGGIKEVIKHGETGFVVDVGDCDSASDYAIRLLE
                     DKVLYNKLQKNMLADIAERFGSELITDQYEYYYQKMLNEHNKSKGE"
     gene            complement(10167. .10484)
                     /gene="MW1349"
     CDS             complement(10167. .10484)
                     /gene="MW1349"
                     /note="ORFID:MW1349"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="BAB95214.1"
                     /db_xref="GI:21204518"
                     /translation="MKSMVEMQREVDEYIGQFKTGYFSPLANLARLTEEVGELAREIN
                     HTYGEKKKKDSEEANTIKAELGDNLFVLLCLANSMGIDMTESFNETMEKFNTRDKNRF
                     ERK"
     gene            complement(10820. .11518)
                     /gene="MW1350"
     CDS             complement(10820. .11518)
                     /gene="MW1350"
                     /note="ORFID:MW1350"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="BAB95215.1"
                     /db_xref="GI:21204519"
                     /translation="MSSIFTMIIYFVILMVLPLWAQHKVKSNYEKYSQVRSTSGKTGR
                     EVALEILHANGIYDVEVVKGEGFLTDHYDPKKKVVSLSPANYDRPSVAGTAIAAHEVG
                     HAIQDHQGYWFLRFRAALVPVANLGSSLSYMIIMLGIILTAIGSAFGSTALWIGAGLM

  Query Match          100.0%;  Score 387;  DB 1;  Length 333750;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-77;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23844 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 23903

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23904 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 23963

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23964 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 24023

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24024 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 24083

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24084 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 24143

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24144 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 24203

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||||||||||||||||||||||
Db      24204 TTAACCATTCACCTGAAGAATAAATAC 24230
```

```
RESULT 4
AP003362
LOCUS       AP003362              346900 bp    DNA     linear   BCT 07-FEB-2002
DEFINITION  Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete
            sequence, section 5/9.
ACCESSION   AP003362 BA000017
VERSION     AP003362.2  GI:14247083
KEYWORDS    .
SOURCE      Staphylococcus aureus subsp. aureus Mu50
  ORGANISM  Staphylococcus aureus subsp. aureus Mu50
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1
  AUTHORS   Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
            Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
            Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
            Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
            Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
            Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C.,
            Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K.
  TITLE     Whole genome sequencing of meticillin-resistant Staphylococcus
            aureus
  JOURNAL   Lancet 357 (9264), 1225-1240 (2001)
  MEDLINE   21311952
   PUBMED   11418146
REFERENCE   2  (bases 1 to 346900)
  AUTHORS   Ohta,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
            of Medical Technology and Nursing, Department of Medical
            Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan
            (E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
            Fax:81-298-53-3454)
COMMENT     On May 29, 2001 this sequence version replaced gi:13875626.
FEATURES             Location/Qualifiers
     source          1. .346900
                     /organism="Staphylococcus aureus subsp. aureus Mu50"
                     /mol_type="genomic DNA"
                     /strain="Mu50"
                     /sub_species="aureus Mu50"
                     /db_xref="taxon:158878"
     gene            12. .263
                     /gene="SAV1313"
     CDS             12. .263
                     /gene="SAV1313"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB57475.1"
                     /db_xref="GI:14247084"
                     /translation="MLTLIKLKEDEQVIIYEYIPEDDISNGKGSVTFNKKDAEVIDFS
                     LSEIENEEYFMLYRNKSFSVVRDFIEKQEFPENYKIAWY"
     gene            987. .1181
                     /gene="SAV1314"
     CDS             987. .1181
                     /gene="SAV1314"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB57476.1"
                     /db_xref="GI:14247085"
                     /translation="MNLQSYIGKLVKLTLTNNKILIGKVIDFDDKVDNFDGYNSIEID
                     TGRITYDISENKIKTIVLQK"
     gene            complement(1725. .2750)
                     /gene="SAV1315"
     CDS             complement(1725. .2750)
                     /gene="SAV1315"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="BAB57477.1"
                     /db_xref="GI:14247086"
```

```
                     /translation="MISFENDYLEGAHEKVLKRLVDTNLVQASGYGFDQFTAQAIEKI
                     KDTIDCPNATIRFLVGGTQTNQVVINSMLESYEGVISADTGHVAVHEGGAIEYSGHKV
                     ITIPSKEGKVSASDVETYMETFKSDFKKDHMVFPGMVYISHPTEYGTLYSKSELEELC
                     KVCKQYQLPLFMDGARLGYGLMSDQSDMTIKDIAKYCDVFYIGGTKIGALCGEAIVFT
                     KNNEPKQFTTRIKHHGALLAKGRLTGIQFLELFTDNLYFNISRHAIEMANKMKDGFKN
                     KGYRLYFDSPTNQQFFILSNEKIAELEQKVKFAVWEKYDDQHRVVRFATSWATTEENL
                     NKLLELI"
gene                 3020. .3217
                     /gene="SAV1316"
CDS                  3020. .3217
                     /gene="SAV1316"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB57478.1"
                     /db_xref="GI:14247087"
                     /translation="MEQIKLKTFTAETLELLEKNINAFLSSEEATNLKLVNITIKEIE
                     ERTFPNNEEEFNAILTLSVNK"
gene                 3238. .4755
                     /gene="SAV1317"
CDS                  3238. .4755
                     /gene="SAV1317"
                     /codon_start=1
                     /transl_table=11
                     /product="cardiolipin synthetase homolog"
                     /protein_id="BAB57479.1"
                     /db_xref="GI:14247088"
                     /translation="MFFVPFFIGEKTMRYTFSNDLGTLFTIILAIGFIINLVLAFIII
                     FLERNRRTASSTWAWLFVLFVLPLIGFILYLFFGRTVSARKLNKNNGNVLTDFDGLLK
                     QQIESFDKGNYGTDNKQVQKHHDLVSMLLMDQDGFLTENNKVDHFIDGNDLYDQVLKD
                     IKNAKEYIHLEYYTFALDGLGKRILHALEEKLKQGLEVKILYDDVGSKNVKMANFDHF
                     KSLGGEVEAFFASKLPLLNFRMNNRNNHRKIIVIDGQLGYVGGFNIGDEYLGLGKLGYW
                     RDTHLRIQGDAVDALQLRFILDWNSQAHRPQFEYDVKYFPKKNGPLGNSPIQIAASGP
                     ASDWHQIEYGYTKMIMSAKKSVYLQSPYFIPDNSYINAIKIAAKSGVDVHLMIPCKPD
                     HPLVYWATFSNASDLLSSGVKIYTYENGFIHSKMCLIDDEIVSVGTANMDFRSFELNF
                     EVNAFVYDENLAKDLRVAYEHDITKSKQLTKESYANRPLSVKFKESLAKLVSPIL"
gene                 4939. .5436
                     /gene="SAV1318"
CDS                  4939. .5436
                     /gene="SAV1318"
                     /note="ATP-binding protein"
                     /codon_start=1
                     /transl_table=11
                     /product="ABC transporter homolog"
                     /protein_id="BAB57480.1"
                     /db_xref="GI:14247089"
                     /translation="MIQISNINKSFNKRCVLKNISFDIEQGKCIALIGKNGAGKSTLI
                     DILIGNVNANSGEIFDKDKLLQSENRSIMFQKTMFPDQLKVIEIINLYQSFYENPLPL
                     EEIIELTKFDSSQLNQFVNKLSGGQQRLLDFVLSLIGQPQLILLDEPTSTMDIEIREY
                     FWSII"
gene                 5461. .5838
                     /gene="SAV1319"
CDS                  5461. .5838
                     /gene="SAV1319"
                     /note="ATP-binding protein"
                     /codon_start=1
                     /transl_table=11
                     /product="ABC transporter homolog"
                     /protein_id="BAB57481.1"
                     /db_xref="GI:14247090"
                     /translation="MLYTSHYIEEVERMSDKIILIENGEIILNDSTSHIRTNQQSQIT
                     LSDEYIRKLKLDKDDLVIQKNHNGTIKIITSNVNDTILYLQQLHINLDDIEIQKVSIV
                     DSYFNNKKQRGSNYDTKLLENRI"
gene                 5807. .6538
                     /gene="SAV1320"
CDS                  5807. .6538
                     /gene="SAV1320"
                     /note="similar to ABC transporter integral membrane
                     protein"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB57482.1"
                     /db_xref="GI:14247091"
                     /translation="MILSYLKIEFKVIMRKKTTLILSILFPVIFYILFTSILELPEDV
                     KPKFYKEYMYSMTVYSLLSFSLLTFPLDIINEKQNEWRQRLMVTPFTFTSYYISKVVK
                     TMLQFAIAILVIFMVGHFYKGVAMSAVQWLESGIFLWLGASLLITFGILFSLLNDIQK
                     TSALANIVTIGLAVLGGLWFPINTFPNWLQHVAHVLPSYHLRKLGVDIASNHHINLIS
                     FAIILLYVLGSIIAVYCISHFKRAE"
gene                 6542. .7633
                     /gene="SAV1321"
CDS                  6542. .7633
                     /gene="SAV1321"
                     /note="similar to two-component sensor histidine kinase"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB57483.1"
                     /db_xref="GI:14247092"
                     /translation="MKFLKDTSIAEISSILYLIFPIAGIFFNEVYGPKWLYIISVIVF
                     SLSYLILVIVNNRLNTLMFYILLIIHYFIICYFVFSVHPMLSLFFFYSAFAVPFTFKN
                     NVKKTATNLFILTMIICTIITYLLYNNYFVAMMVYYVVISLIMLDNFKKMKNREYQKE
                     IAEKNRHINTLIAEQERHRIGQDLHDTLGHVFASLSLKSELAYKLIDTDVEKVKAELL
                     AINKLSRESLNKVREIIDDVKLPSFIEEIDSIRKVLKDADIDFTFENKELAQVLSPTK
                     QSMLVMITREAINNVIKHANASKVHGKLKTVNNHKLLLMIEDDGKGIDSDCEVKSISQ
                     RVQHLNGTLAVDSTNGTKIIIEISTGGIA"
gene                 7630. .8232
                     /gene="SAV1322"
CDS                  7630. .8232
                     /gene="SAV1322"
                     /note="similar to two-component response regulator"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB57484.1"
                     /db_xref="GI:14247093"
                     /translation="MTSLIIAEDQNMLRQAMVQLIKLHGDFEILADTDNGLDAMKLIE
                     EYNPNVVILDIEMPGMTGLEVLAEIRKKHLNIKVIIVTTFKRPGYFEKAVVNDVDAYV
                     LKERSIEELVETINKVNNGEKEYSATLMTSFFVDKNPLTPKEQIVLREIGNGLSSKEI
                     SEKLFLTDGTVRNYTSVIIDKLFADNRFDAWKKANEKGWI"
gene                 complement(8345. .8533)
                     /gene="SAV1323"
CDS                  complement(8345. .8533)
                     /gene="SAV1323"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="BAB57485.1"
                     /db_xref="GI:14247094"
                     /translation="MNISNENTVTLIAVIIAIIIGIFLQIFFKLPLIVTAVLSILLGI
                     FVGFIVYLIVSFYNKRKN"
gene                 8672. .9205
                     /gene="nuc"
CDS                  8672. .9205
                     /gene="nuc"
                     /note="SAV1324"
                     /codon_start=1
                     /transl_table=11
                     /product="thermonuclease"
                     /protein_id="BAB57486.1"
                     /db_xref="GI:14247095"

 Query Match          100.0%;  Score 387;  DB 1;  Length 346900;
 Best Local Similarity  100.0%;  Pred. No. 1.2e-77;
 Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200303 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 200362

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200363 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 200422

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db     200423 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 200482

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200483 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 200542

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200543 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 200602

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200603 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 200662

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||||||||||||||||||||||
Db     200663 TTAACCATTCACCTGAAGAATAAATAC 200689


RESULT 5
AF270032
LOCUS       AF270032               3269 bp    DNA     linear   BCT 01-AUG-2000
DEFINITION  Staphylococcus epidermidis strain SR1 clone step.1042f07 genomic
            sequence.
ACCESSION   AF270032
VERSION     AF270032.1  GI:9623936
KEYWORDS    .
SOURCE      Staphylococcus epidermidis
  ORGANISM  Staphylococcus epidermidis
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1  (bases 1 to 3269)
  AUTHORS   Kimmerly,W.J., Taylor,J.David., Nelsen,A.J., Godlevski,M.M.,
            Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
            Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
            Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
            Furdon,P.J.
  TITLE     Transposon-mediated sequencing of the Staphylococcus epidermidis
            genome
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3269)
  AUTHORS   Taylor,J.David., Kimmerly,W.J., Nelsen,A.J., Godlevski,M.M.,
            Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
            Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
            Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
            Furdon,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAY-2000) Departments of Genomic Sciences and
            Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
            Drive, Research Triangle Park, North Carolina 27709-3398, USA
FEATURES             Location/Qualifiers
     source          1. .3269
                     /organism="Staphylococcus epidermidis"
                     /mol_type="genomic DNA"
                     /strain="SR1"
                     /db_xref="taxon:1282"
                     /clone="step.1042f07"
BASE COUNT      986 a    616 c    451 g   1216 t
ORIGIN

  Query Match             67.8%;  Score 262.2;  DB 1;  Length 3269;
  Best Local Similarity   79.8%;  Pred. No. 3.1e-49;
  Matches  309;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||   |||| |  ||| |    ||||||||||||| ||| || ||||| ||||
Db       2297 GATCTTCTGATTCTTTATTAAAGTTTTCAACAACTGCATCTAGCAAATCTCCAAGTCCTA 2356

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              | ||||||||  || || || ||||| || || ||||| ||||| ||||||||||||| |
Db       2357 ATCCATGTGAACCAGAAATAGGATATGGATCTCCAAAGCCTAAAGAATAGAAATCATAGA 2416

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
               ||  |||||||||| | |||||| ||||| || || |||||||| || ||||| ||||
Db     200423 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 200482

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              |||| || |  ||||| |||||||||| || |||||||| | |||||| |  || || |
Db     200483 ATTTGTATAAAGCATTTGTGCGACCATTTCGTCACTTTGTGTAAGTCCTTCTCTAACATTGA 200542

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              |||||||||| || ||||| ||||| || || || |||||||||| || |  ||||| |
Db     200543 CCATAAAAATGATGACATCTGCTTCTTCAATTGCTATTTCTGCCTGTGCACGGATTTGAG 200602

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              |||| || || ||||| |||||||||||||||||||||||||| || || || ||||| |
Db     200603 TTTGAAAAGGAGCATCTCCAATTTCAATACCACCTGTATCAATGATGTTAAATTCATGAG 200662

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||| || || || ||||||||||
Db     200663 TTAACCACTCGCCAGATGAATAAATAC 200689


RESULT 6
AX145350
LOCUS       AX145350               3269 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 4072 from Patent WO0134809.
ACCESSION   AX145350
VERSION     AX145350.1  GI:14283915
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kimmerly,W.J.
  TITLE     Staphylococcus epidermidis nucleic acids and proteins
  JOURNAL   Patent: WO 0134809-A 4072 17-MAY-2001;
            GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .3269
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid sequence"
BASE COUNT      986 a    616 c    451 g   1216 t
ORIGIN

  Query Match             67.8%;  Score 262.2;  DB 6;  Length 3269;
  Best Local Similarity   79.8%;  Pred. No. 3.1e-49;
  Matches  309;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||   |||| |  ||| |    ||||||||||||| ||| || ||||| ||||
Db       2297 GATCTTCTGATTCTTTATTAAAGTTTTCAACAACTGCATCTAGCAAATCTCCAAGTCCTA 2356

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              | ||||||||  || || || ||||| || || ||||| ||||| ||||||||||||| |
Db       2357 ATCCATGTGAACCAGAAATAGGATATGGATCTCCAAAGCCTAAAGAATAGAAATCATAGA 2416

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
               ||  |||||||||| | |||||| ||||| || || |||||||| || ||||| ||||
Db       2417 TATCATTACGCATTTCAAGATTATCAACTTTATTCACAGCTAATACAACAGGTTTCTTAG 2476

Qy        181 ATTTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              |||| || |  ||||| |||||||||| || |||||||| | |||||| |  || || |
Db       2477 ATTTATAAAGCATTTGTGCGACCATTTCGTCACTTTGTGTAAGTCCTTCTCTAACATTGA 2536

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              |||||||||| || ||||| ||||| || || || |||||||||| || |  ||||| |
Db       2537 CCATAAAAATGATGACATCTGCTTCTTCAATTGCTATTTCTGCCTGTGCACGGATTTGAG 2596

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              |||| || || ||||| |||||||||||||||||||||||||| || || || ||||| |
Db       2597 TTTGAAAAGGAGCATCTCCAATTTCAATACCACCTGTATCAATGATGTTAAATTCATGAG 2656

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||| || || || ||||||||||
```

```
Db       2657 TTAACCACTCGCCAGATGAATAAATAC 2683


RESULT 7
AE016747
LOCUS       AE016747               300892 bp    DNA     linear   BCT 01-JAN-2003
DEFINITION  Staphylococcus epidermidis ATCC 12228, section 4 of 9 of the
            complete genome.
ACCESSION   AE016747 AE015929
VERSION     AE016747.1  GI:27315369
KEYWORDS    .
SOURCE      Staphylococcus epidermidis ATCC 12228
  ORGANISM  Staphylococcus epidermidis ATCC 12228
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1  (bases 1 to 300892)
  AUTHORS   Zhang,Y., Ren,S., Li,H., Fu,G., Lu,L., Lu,G., Jia,J., Tu,Y.,
            Qin,Z., Chen,Z. and Wen,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2002) Chinese National Human Genome Center at
            Shanghai, 250 Bi Bo Road, Shanghai 201203, China
FEATURES             Location/Qualifiers
     source          1. .300892
                     /organism="Staphylococcus epidermidis ATCC 12228"
                     /mol_type="genomic DNA"
                     /strain="ATCC 12228"
                     /db_xref="ATCC:12228"
                     /db_xref="taxon:176280"
     gene            113. .346
                     /locus_tag="SE0907"
     CDS             113. .346
                     /locus_tag="SE0907"
                     /codon_start=1
                     /transl_table=11
                     /product="acyl carrier protein"
                     /protein_id="AAO04504.1"
                     /db_xref="GI:27315370"
                     /translation="MENFDKVKDIIVDRLGVDADKVTEDASFKDDLGADSLDIAELVM
                     ELEDEFGTEIPDEEAEKINTVGDAVKYINSLEK"
     gene            461. .1198
                     /locus_tag="SE0908"
     CDS             461. .1198
                     /locus_tag="SE0908"
                     /codon_start=1
                     /transl_table=11
                     /product="RNase III"
                     /protein_id="AAO04505.1"
                     /db_xref="GI:27315371"
                     /translation="MANQKKKEMVHNFQQKFTDKMKSLGLHFKNIDLYQQAFSHSSFI
                     NDFNMNRLEHNERLEFLGDAVLELTVSRYLFDRHPHLPEGNLTKMRATIVCEPSLVIF
                     ANKIKLNELILLGKGEEKTGGRTRPSLISDAFEAFVGALYLDQGLDSVWTFAEKVIFP
                     YVEDDELVGVVDFKTQFQEYVHSQNKGDVTYQLIKEEGPAHHRLFTSEVILENKAVAE
                     GKGKTKKESEQKAAEQAYKLMKNKKSL"
     gene            1325. .4894
                     /locus_tag="SE0909"
     CDS             1325. .4894
                     /locus_tag="SE0909"
                     /codon_start=1
                     /transl_table=11
                     /product="chromosome segregation SMC protein"
                     /protein_id="AAO04506.1"
                     /db_xref="GI:27315372"
                     /translation="MVYLKSIDAIGFKSFADHTNVQFDKGVTAIVGPNGSGKSNITDA
                     IKWVLGEQSAKSLRGAKMEDIIFSGAEHRKAQNFAEVKLKLDNHSQKLQIDSEELVVT
                     RRLYRSGESEYYLNNDRARLKDIIDLFLDSGLGKEAFSIISQGRVDEILNAKPINRRQ
                     IIEESAGVLKYKKRKAESIQKLDHTEDNLNRVEDILYDLEGRVEPLKEEAAIAKEYKQ
                     LSKEMEQSDVIVTVSDIDHYTEDNQRLDERLNHLKSQQAEKEGQQAQINQLLQKYKGK
                     RQQNDYDIEKLNYELVKATENYEQLSGKLNVLEERKKNQSETNARYEEELDNLESQID
                     SIKNEKAQNEKLLAELKNKQKQLNKEVQELESLLYISDEQHDEKLEEIKNSYYTLMSE
                     QSDVNNDIRFLEHTINENEAKKSRLDSRLVEAFNQLKDIQQNITQTQKEYQSSKKSME
                     KVEQNIQQLEQQLTDSKRLLSEYENKLYQAYRYNEKLKSRIDSLATQEEDYTYFFNGV
                     KHILKAKDKELRGIHGAVAEVINVPSEMTQAIETALGASLQHVIVDNEKDGRQAIQYL
                     KQRGLGRATFLPLNVIQPRHVAADIKDVARGSQGFINIASDAINVSAKYQNIIENLLG
                     NTIIVENLKHANELARAIRYRTRIVTLEGDVVNPGGSMTGGGARKTKSILSQKDELST
                     MRNQLEDYQRQTAEFERQFKEQKTQAEQLSEQYFSASQQYNNLKEQVHHHELELDRLK
                     TQEAHLKNEHEEFEFEKNDGYQSDKSKETLKEKQNHLIEIQQQLKQLESDIERYTQLS
                     KEGKASTHQTQQQLHQKQSDLAVVKERIKSQKQVYERLDKQLSDSERQKIEVNEKIKL
                     FNSDEMMGKDAFEKLKEQIQQQENVRQNLNQQLSEIKQQRKDLNEKIEINESQLQKCH
                     QDILSIENHYQDIKAKQSKLDVLINHAIDHLNDTYQLTVERARMEYDSDETIDNLRKK
                     VKLTKMSIDELGPVNLNAIEQFEELNERYTFLNEQRTDLREAKETLEQIIHEMDKEVE
                     GRFKTTFHAVQDHFTTVFKQLFGGGQAELRLTEDDYLSAGVDIIVQPPGKKLQHLSLL
                     SGGERALSAIALLFAILKVRSAPFVILDEVEAALDEANVIRYAQYLNELSTETQFIVI
                     THRKGTMEFSDRLYGVTMQESGVSKLVSVNLNTIDEVMKEEQA"
     gene            4891. .6117
                     /locus_tag="SE0910"
     CDS             4891. .6117
                     /locus_tag="SE0910"
                     /codon_start=1
                     /transl_table=11
                     /product="signal recognition particle"
                     /protein_id="AAO04507.1"
                     /db_xref="GI:27315373"
                     /translation="MSFFKRLKDKFSSKSEDDIQKDLDETVDSNANSDSDSMDPNDSD
                     EQVKPKKKPKKLSEADFDEDGLISIEDFEEIEAQKIGAKFKAGLEKSRQNFQEQLNNL
                     IARYRKVDEDFFEALEEMLITADVGFNTVMKLTDELRTEAQRRNIQETEDLREVIVEK
                     IVEIYHQEDDHSEAMNIEDGRLNVILMVGVNGVGKTTTIGKLAYRYQQEGKKVMLAAG
                     DTFRAGAIQQLNVWGERVGVEVVSQNEGSDPAAVVYDAINAAKNKGVDILICDTAGRL
                     QNKSNLMQELDKMKRVINRAIPDAPHEALLCLDATTGQNALSQARSFKEVTNVSGIVL
                     TKLDGTAKGGIVLAIRNELHIPVKYVGLGEKMDDLQPFNPESYVYGLFADMIEQNEDI
                     PEEISRNSSVESEEGN"
     gene            6119. .6451
                     /locus_tag="SE0911"
     CDS             6119. .6451
                     /locus_tag="SE0911"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="AAO04508.1"
                     /db_xref="GI:27315374"
                     /translation="MGQNDLVKTLRMNYLFDFYQSLLTNKQKNYLEFFYLQDYSLSEI
                     ADTFEVSRQAVYDNIRRTGDLVEDYESKLRLYQRFEKRRELYNLMKQSLNQPELLKQY
                     ITQLEELE"
     gene            6482. .7849
                     /locus_tag="SE0912"
     CDS             6482. .7849
                     /locus_tag="SE0912"
                     /codon_start=1
                     /transl_table=11
                     /product="ffh protein"
                     /protein_id="AAO04509.1"
                     /db_xref="GI:27315375"
                     /translation="MAFEGLSDRLQATMQKMRGKGKVTEADIKTMMREVRLALLEADV
                     NFKVVKEFVKTVSERALGSDVMQSLTPGQQVIKIVQEELTSLMGGENTSIKMANKPPT
                     VVMMVGLQGAGKTTTAGKLALLMRKKYNKKPLLVAGDIYRPAAIDQLQTVGKQIDIPV
                     YSEGDQVSPQQIVENALKHAKEEHLDFVIIDTAGRLHIDEALMNELQEVKEISKPDEI
                     MLVVDAMTGQDAVNVAQSFDEQLDVSGVTLTKLDGDTRGGAALSIRSVTQKPIKFVGM
                     SEKLDGLELFHPERMASRILGMGDVLSLIEKAQQDVDQEKAKDLEKKMRESSFTLDDF
                     LEQLDQVKNLGPLDDIMKMIPGMNKMKGLDKLNMSDKQIDHIKAIIQSMTPKERSNPE
                     TLNVSRKKRIAKGSGRSLQEVNRLMKQFNDMKKMMKQFTGGGKGKKAKRNQMQNMLKG
                     MNLPF"
     gene            8281. .8556
                     /locus_tag="SE0913"
     CDS             8281. .8556
                     /locus_tag="SE0913"
                     /codon_start=1
                     /transl_table=11
                     /product="30S ribosomal protein S16"
                     /protein_id="AAO04510.1"
                     /db_xref="GI:27315376"
                     /translation="MAVKIRLTRLGSKRNPFYRIVVADARSPRDGRIIEQLGTYNPAH
                     VNAPEVKIDEELALKWLHDGAKPTDTVHNILSREGILKKFDEQKNAK"
     gene            8683. .9186
                     /locus_tag="SE0914"
     CDS             8683. .9186
                     /locus_tag="SE0914"
                     /codon_start=1
                     /transl_table=11
```

```
                     /product="rimM protein"
                     /protein_id="AAO04511.1"
                     /db_xref="GI:27315377"
                     /translation="MEVEVGQIVNTHGIKGEVKVKSNSDFTETRFQPGEQLLVKHNNT
                     EIVYTVASYRIHKGFHMLRFEGINNINEIEHLKGDYIYQERDHQDIELGEHEYYYSDI
                     IGCTVFKDDDTPIGRVINIFETGANDVWVVKGEKEYLIPYIEDVVKDIDIETKTIKIT
                     PMEGLLD"
          gene       9186. .9923
                     /locus_tag="SE0915"
          CDS        9186. .9923
                     /locus_tag="SE0915"
                     /codon_start=1
                     /transl_table=11
                     /product="tRNA (guanine-N1)-mehtyltransferase"
                     /protein_id="AAO04512.1"
                     /db_xref="GI:27315378"
                     /translation="MKIDYLTLFPEMFEGVLNHSILKRAQDKGIINVNTINFRDYSIN
                     KHNQVDDYPFGGGQGMVLKPEPVFNAMEDINHNEHTRVILMCPQGRPFTQEIAQELSE
                     AKHIVFICGHYEGYDERIRKHLVTDEISMGDYVLTGGELPAMTMTDAIVRLIPGVLGN
                     QASHQDDSFSDGLLEFPQYTRPREYKNMSVPEVLLSGNHAHIDQWRHEQKLIRTYEKR
                     PDLLEQYPLTEKDREILETYKKKLKND"
          gene       10029. .10379
                     /locus_tag="SE0916"
          CDS        10029. .10379
                     /locus_tag="SE0916"
                     /codon_start=1
                     /transl_table=11
                     /product="50S ribosomal protein L19"
                     /protein_id="AAO04513.1"
                     /db_xref="GI:27315379"
                     /translation="MSNHKLIEAVTKSQLRTDLPTFRSGDTLRVHVRIVEGSRERIQV
                     FEGVVIKRRGGGISETFTVRKISSGVGVERTFPLHTPKIEKIEVKRRGKVRRAKLYYL
                     RSLRGKAARIQEIR"
          gene       complement(10910. .13513)
                     /locus_tag="SE0917"
          CDS        complement(10910. .13513)
                     /locus_tag="SE0917"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="AAO04514.1"
                     /db_xref="GI:27315380"
                     /translation="MIKNIWNKPIKRFTLIVLVSCILSFILYGPFLYQFITKGIVFSG
                     SGDGFRQMMPFQMHLYEHFTSLKGFYDASFGLGGDYVKSLAYYYSLSPLMWINFSMIW
                     ILEQTINVNPHDISFWTINQLIMAYVRTVITFIFSFYLFSYLRLKPAPMFIATILYGM
                     STVVTYYNFTWSFYGNLLIMLPMSLWAIERFFKERKIGWFIFAIAYTLFSNFYFSYYE
                     AIVIGFYFIYRFAIPHEKDIVNRWQKLYILVCATLLSVLVSIYGLYTGVSSFLDNDRT
                     QNPNFKITFFTNLFETNYNIFADGFYITISFIAIIALFCFKLYQHYYYKLFAIATWIL
                     LIGSFSQWFDSAFNGFSLPQRRWVYFLALSTSVLIALFIQHLSEISIKEYTFVAIPVF
                     IYGFIFIALSERSVKWMFVALILIIVLFIFIKYKSLLTRTSMMVLLVVLFLAQQVLMT
                     NDSRKITIEPYQTTIKTINDSSYRSPVLNKKIKYMHQSSTDPLKRLDYFSYYALNSPL
                     IYHYNGTSLYSSIFDGDILKYYDQTLQINMPVDKNSTYRYLNNRANLMSLWDVQDRLR
                     HPDDLNMPYGFKKKELITDKKDQWIHSVNTINYPSAHITNKIYDARKLKSPLDREQAM
                     LKGVVLNHKSQANTDFKPNPNLLSNAKQNLNHANWIDSKHLKVKQHNGGVTLNLPRNI
                     VKNYKDMYIEMDVELLSPDKEHKVGVNEYSQERNRLSYKYRRFVSPVTMRAKASNQLN
                     IKMSKGVYRFKVKGIYGENYQTLKKASQQLQPVKVKKERNGFTIIKKKKEHGYLVLPM
                     VYAEGMHAMANGKPLKVQQGNGIMTTIPVKEGQTKIKLSYTPPYFYLLITVSCIGIIL
                     SILFTHYVKRK"
          gene       complement(13506. .15779)

  Query Match          67.8%;  Score 262.2;  DB 1;  Length 300892;
  Best Local Similarity  79.8%;  Pred. No. 2e-49;
  Matches  309;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy          1 GATCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTA 60
              ||||||||   |||| |  ||| |    ||||||||||||||| ||| || ||||| ||||
Db     296677 GATCTTCTGATTCTTTATTAAAGTTTTCAACAACTGCATCTAGCAAATCTCCAAGTCCTA 296736

Qy         61 AACCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACA 120
              | ||||||||  || || || ||||| || || ||||| ||||| ||||||||||||||| |
Db     296737 ATCCATGTGAACCAGAAATAGGATATGGATCTCCAAAGCCTAAAGAATAGAAATCATAGA 296796

Qy        121 CGTCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAG 180
              ||  |||||||||| | |||||| ||||| || || |||||||| || ||||| ||||
Db     296797 TATCATTACGCATTTCAAGATTATCAACTTTATTCACAGCTAATACAACAGGTTTCTTAG 296856

Qy        181 ATTTGTATAAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAA 240
              |||| || |  ||||| |||||||||| || |||||||| | |||||| |  || || |
Db     296857 ATTTATAAAGCATTTGTGCGACCATTTCGTCACTTTGTGTAAGTCCTTCTCTAACATTGA 296916

Qy        241 CCATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTG 300
              |||||||||| || ||||| ||||| || || || |||||||||| || |  |||||  |
Db     296917 CCATAAAAATGATGACATCTGCTTCTTCAATTGCTATTTCTGCCTGTGCACGGATTTGAG 296976

Qy        301 TTTGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTG 360
              |||| || || ||||| |||||||||||||||||||||||||| || || || ||||| |
Db     296977 TTTGAAAAGGAGCATCTCCAATTTCAATACCACCTGTATCAATGATGTTAAATTCATGAG 297036

Qy        361 TTAACCATTCACCTGAAGAATAAATAC 387
              ||||||| || || || ||||||||||
Db     297037 TTAACCACTCGCCAGATGAATAAATAC 297063


RESULT 8
AE017028/c
LOCUS       AE017028              290117 bp    DNA     linear   BCT 30-APR-2003
DEFINITION  Bacillus anthracis str. Ames section 5 of 18 of the complete
            genome.
ACCESSION   AE017028 AE016879
VERSION     AE017028.1  GI:30255149
KEYWORDS    .
SOURCE      Bacillus anthracis str. Ames
  ORGANISM  Bacillus anthracis str. Ames
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1  (bases 1 to 290117)
  AUTHORS   Read,T., Peterson,S., Tourasse,N., Baillie,L., Paulsen,I.,
            Nelson,K., Tettelin,H., Fouts,D., Eisen,J., Gill,S., Holtzapple,E.,
            Okstad,O., Helgason,E., Rilstone,J., Wu,M., Kolonay,J., Beanan,M.,
            Dodson,R., Brinkac,L., Gwinn,M., DeBoy,R., Madupu,R., Daugherty,S.,
            Durkin,A., Haft,D., Nelson,W., Peterson,J., Pop,M., Khouri,H.,
            Radune,D., Benton,J., Mahamoud,Y., Jiang,L., Hance,I., Weidman,J.,
            Berry,K., Plaut,R., Wolf,A., Watkins,K., Nierman,W., Hazen,A.,
            Cline,R., Redmond,C., Thwaite,J., White,O., Salzberg,S.,
            Thomason,B., Friedlander,A., Koehler,T., Hanna,P., Kolsto,A.-B. and
            Fraser,C.
  TITLE     The genome sequence of Bacillus anthracis Ames and comparison to
            closely related bacteria
  JOURNAL   Nature 423 (6935), 81-86 (2003)
  MEDLINE   22608414
   PUBMED   12721629
REFERENCE   2  (bases 1 to 290117)
  AUTHORS   Read,T., Peterson,S., Tourasse,N., Baillie,L., Paulsen,I.,
            Nelson,K., Tettelin,H., Fouts,D., Eisen,J., Gill,S., Holtzapple,E.,
            Okstad,O., Helgason,E., Rilstone,J., Wu,M., Kolonay,J., Beanan,M.,
            Dodson,R., Brinkac,L., Gwinn,M., DeBoy,R., Madupu,R., Daugherty,S.,
            Durkin,A., Haft,D., Nelson,W., Peterson,J., Pop,M., Khouri,H.,
            Radune,D., Benton,J., Mahamoud,Y., Jiang,L., Hance,I., Weidman,J.,
            Berry,K., Plaut,R., Wolf,A., Watkins,K., Nierman,W., Hazen,A.,
            Cline,R., Redmond,C., Thwaite,J., White,O., Salzberg,S.,
            Thomason,B., Friedlander,A., Koehler,T., Hanna,P., Kolsto,A.-B. and
            Fraser,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2003) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .290117
                     /organism="Bacillus anthracis str. Ames"
                     /mol_type="genomic DNA"
                     /strain="Ames"
                     /db_xref="taxon:198094"
          gene       331. .1929
                     /locus_tag="BA1197"
          CDS        331. .1929
                     /locus_tag="BA1197"
                     /note="similar to GP:10717143,  and GP:10717143;
```

```
                identified by sequence similarity; putative"
                /codon_start=1
                /transl_table=11
                /product="oligopeptide ABC transporter,
                oligopeptide-binding protein"
                /protein_id="AAP25159.1"
                /db_xref="GI:30255150"
                /translation="MMLGACSYQKDEPQANAKGDSGKSGAKQVINLTEVSEIPTMDTT
                LASDAASSKVMNNTMEGLYRLGKGDKLVPGVAKSHTKSEDGKKYTFKLREDAKWSNGD
                PVTAKDFVYAWQRAVNPDTAAKSGYIMLDVKNAEKINKRELSPDQLGVKAIDDYTFEV
                ELDNPVPYFLDLTVYPLFFPLNEKYMKEQGEKFGLEANTTLYNGPFVLNEWKHEQSFQ
                LKKNPSYWDQKEVKLEEVNFNVVKDTGAAVNLYNTSAIDRVGLSAELVDKYKGQQDFK
                TINDPTVFFLRFNQKNPALANKNIRKAISSAYDRDGIGEVILNNGSKGAYGLVPSDFV
                KGPDKQDFRKENGKLSKVDVKEAKKFWEAGKKELGKDKIEIEFLNFDNEESKKIGEYV
                KGELEKNLPGLTVTIKMQPFAQKLKLEDSGQFDISFTGWGPDFPDAITFLDMFITDGS
                QNKMGYSNAEYDSLIKKAKQEGSDVKGRWNDLLKAEKILFEDAAIAPVFQRGRSILER
                ETIKDVYIHKYGGELSFKWASVEK"
gene            complement(1956. .2099)
                /locus_tag="BA1198"
CDS             complement(1956. .2099)
                /locus_tag="BA1198"
                /note="identified by Glimmer2; putative"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein"
                /protein_id="AAP25160.1"
                /db_xref="GI:30255151"
                /translation="MIGVITNSIGEKLFGGKEKMKFVNKSLDVQSGWNEVGGKGIYKK
                RTY"
gene            2731. .3126
                /locus_tag="BA1200"
CDS             2731. .3126
                /locus_tag="BA1200"
                /note="similar to SP:P32687, PID:409796, GB:U00096,
                PID:1790459, SP:P32687, PID:409796, GB:U00096,  and
                PID:1790459; identified by sequence similarity; putative"
                /codon_start=1
                /transl_table=11
                /product="conserved hypothetical protein"
                /protein_id="AAP25161.1"
                /db_xref="GI:30255152"
                /translation="MVTLYSSPSCTSCRKAKLWLEENHIPYTERNIFSDPLTIEEIKE
                ILRMTESGTDEIISTRSKVFQELNVNLESLPLQDLYKMIRDYPGILRRPIMIDEKRLQ
                VGYNEDEIRRFLPRTVRTFQLREAQRLVN"
gene            complement(3176. .3850)
                /locus_tag="BA1201"
CDS             complement(3176. .3850)
                /locus_tag="BA1201"
                /note="identified by match to PFAM protein family HMM
                PF03772"
                /codon_start=1
                /transl_table=11
                /product="membrane protein, putative"
                /protein_id="AAP25162.1"
                /db_xref="GI:30255153"
                /translation="MDLEFLTSVLMIVGIDVVLGGDNAIVIALASRNLPESKRNKAIL
                IGTLLAIVLRIILTILAVYLLDIPFLQLIGGVLLTLIAVNLLTDNSNDLSSIQGKTTL
                FQAVRTIVFADLVMGFDNVIAIAGAAHGRFSLVIIGLLISIPIIIWGSKLILMLMERF
                PFLIYCGAAILAYTAGKMVTHEDRLATFFHNNPSFTAGIPYLFIFTILCIGFIVQQVR
                LRNVKH"
gene            4112. .4210
                /locus_tag="BA1202"
CDS             4112. .4210
                /locus_tag="BA1202"
                /note="identified by Glimmer2; putative"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein"
                /protein_id="AAP25163.1"
                /db_xref="GI:30255154"
                /translation="MICHMSGESLHNNSKQEGRVVFWILKELMIIR"
gene            4207. .4860
                /gene="mecA"
                /locus_tag="BA1203"
CDS             4207. .4860
                /gene="mecA"
                /locus_tag="BA1203"
                /note="similar to GB:X03350, GB:X03350, GB:X03350,
                GB:D00137, GB:M21692, GB:M24317, GB:M24308, GB:M24309,
                GB:M24310, GB:M24311, GB:M24312, GB:M24313, GB:M24314,
                GB:M24315, GB:M24316, GB:M37067, GB:X15447, GB:X15448,
                GB:X15449, GB:X15450, GB:X15451, GB:X15452, GB:X15453,
                GB:X15454, GB:X15455, SP:P00325, SP:P00326, SP:P07327,
                PID:1223739, PID:178098, PID:178100, PID:178111,
                PID:219428, PID:28416, PID:598143, PID:825622, GB:X03350,
                GB:X03350, GB:X03350, GB:D00137, GB:M21692, GB:M24317,
                GB:M24308, GB:M24309, GB:M24310, GB:M24311, GB:M24312,
                GB:M24313, GB:M24314, GB:M24315, GB:M24316, GB:M37067,
                GB:X15447, GB:X15448, GB:X15449, GB:X15450, GB:X15451,
                GB:X15452, GB:X15453, GB:X15454, GB:X15455, SP:P00325,
                SP:P00326, SP:P07327, PID:1223739, PID:178098, PID:178100,
                PID:178111, PID:219428, PID:28416, PID:598143, PID:825622,
                GB:X03350, GB:X03350, GB:X03350, GB:D00137, GB:M21692,
                GB:M24317, GB:M24308, GB:M24309, GB:M24310, GB:M24311,
                GB:M24312, GB:M24313, GB:M24314, GB:M24315, GB:M24316,
                GB:M37067, GB:X15447, GB:X15448, GB:X15"
                /codon_start=1
                /transl_table=11
                /product="negative regulator of competence MecA"
                /protein_id="AAP25164.1"
                /db_xref="GI:30255155"
                /translation="MKFFITYIDIEDRGFNREEIWYDRERSEELFWEMMDEARDHDDF
                FIDGPLWIQVQAVDKGIEVLVTKAELSKDGQKLELPIGVDKIIDIPLDEGIESLFQQE
                LVEEVEEQAGTNFNEDGTFGFLIKFNDFEDVISLSHRLIFEDIKDELYSFEDRYYVYV
                EFDEVLHDEEEIDRILSIVLEYGEESTLTIHRVSEYGKQIVKEHALETIRNNFPAKT"
gene            4933. .6477
                /gene="cls-2"
                /locus_tag="BA1204"
CDS             4933. .6477
                /gene="cls-2"
                /locus_tag="BA1204"
                /note="similar to SP:O66043, SP:O66043, SP:O66043,
                SP:O66043, SP:O66043,  and SP:O66043; identified by
                sequence similarity; putative"
                /codon_start=1
                /transl_table=11
                /product="cardiolipin synthetase"
                /protein_id="AAP25165.1"
                /db_xref="GI:30255156"
                /translation="MKNTLKLIFFVLLLFALFVSLRMFIDVAFYSDVIGIKDVSILGI
                ISILFTVSAFLIGCVIFLENRHPSKTLTWLIVLGIFPVFGFFAYLLFGQNFRRKRMFQ
                KKALLDEQAFLQYKGHEDYEERILRNHKHQELLFRLADRLGALNISFQTETRTLTNGD
                ETFQAILDGLKRAKHHIHMEYYIVRDDKLGTEIKDILIQKSKEGVVVRFLYDAVGSFK
                LSKSYIEELNDAGVEMIPFFPVRFPILNDKINYRNHRKIVIIDGNEGFVGGLNIGDEY
                LGKDKYFGFWRDTHLYLRGEAVQSLQLIFLQDWFYMTGEAVLAPEYLQAKAVEGEHWG
                GVQLVAGGPDNKWETIKHLYFAMIASARKSIWIATPYFIPDDDILSALKVAALAGIDV
                RLLMPSKPDKRTVFYASRSYFPELLDAGVKIYEYEKGFLHSKVVIVDSDLASIGTANM
                DMRSFHLNFEVNAFLYDTDSIRKLVQDFKDDLEESSEIHVDRFHKRRLHRRIVESTYR
                LLSPLL"
gene            6559. .7803
                /locus_tag="BA1205"
CDS             6559. .7803
                /locus_tag="BA1205"
                /note="identified by Glimmer2; putative"
                /codon_start=1
                /transl_table=11
                /product="conserved hypothetical protein"
                /protein_id="AAP25166.1"
                /db_xref="GI:30255157"
                /translation="MIPIFIAKRENGEKIHLLDHHDEELLHHMRKRESFFCIACGKEV
                LMRLGKQKRWHFAHKKVDSCLAFYEAESTYHMYGKELLYRWFKRQNVHVEIEHYLPEI
                QQRPDIFIERAGRKIAIEYQCANLSIEQLCKRTYSYWQAGIQVIWIIGGNQLKKHSAY
                WMKFSSIMAFSLQSYPQPLLIFFCSKQKSFMKCTFITSFSTSIAFSHIIYLPIETTTF
                EMLFSPVPFQREVLKREWKRRKDYFRQNALPILNYNHKSLLRLLYQCKCNPANFPSEI
                GVPLPSSFAFQTNSFIWQAFLYMKCIGELAVGDCISLKYVCGYIKKYTKRRMLPYFSQ
                HIWKVAVTEYMTFLCYAGVLYKVGMYTYRKIRDAVPLKTGGEIIKHDEICLAHALSLF
```

```
                 EAKFNMRGGKGDIIKTDREGIT"
     gene        7854. .9580
                 /gene="pepF-1"

  Query Match          54.4%;  Score 210.6;  DB 1;  Length 290117;
  Best Local Similarity  71.7%;  Pred. No. 9.2e-38;
  Matches  276;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              ||||||||     |    ||||||     || || ||||||| |||||||| |  |||||
Db     280879 TCTTCTTCAATCTTTGGAAAATGCTGTGCAGCTTCATCTAATAAGTCACCTAATCCTAAT 280820

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              || ||||  ||||| || ||   | || || |||||||||||||| ||||||||||| | |
Db     280819 CCGTGTGTACCTGAGATTGGGAATGGCTCGCCAAATCCTAATGCATAGAAATCATAAATG 280760

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              ||  | |||||||||  ||| || ||||| || || || | ||| || ||||| || ||
Db     280759 TCACTGCGCATTTCCGGATTGTCCACTTTATTTACTGCAAGTACAACTGGTTTATTTGAA 280700

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
              |||||  ||||  || ||   ||||||   |  ||| |  || |||||  | ||   |
Db     280699 CGATATAATATTTTTGCAACTTCTTCATCCGCTGCTGTTACACCGTCACGACCATTTGTC 280640

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||| |||||||| |||||||| || || | ||| || ||    | |||||||||
Db     280639 ATAAAAATGATAACATCTGCTTCATCAATTGCTACTTCAGCTTGTTGACGAATTTGTGTC 280580

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              |||||  | || ||||| ||||| |||||||||||||||| || || |||||  ||
Db     280579 AAAAATGGCTCGTCTCCAATATCAATTCCACCTGTATCAATAATGTTAAATTCATGATTT 280520

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              |||||||| || |    ||||||||
Db     280519 AACCATTCTCCAGCGCTATAAATAC 280495


RESULT 9
AE017002/c
LOCUS       AE017002               304680 bp    DNA     linear   BCT 16-MAY-2003
DEFINITION  Bacillus cereus ATCC 14579 section 5 of 18 of the complete genome.
ACCESSION   AE017002 AE016877
VERSION     AE017002.1  GI:29894935
KEYWORDS    .
SOURCE      Bacillus cereus ATCC 14579
  ORGANISM  Bacillus cereus ATCC 14579
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
            cereus group.
REFERENCE   1  (bases 1 to 304680)
  AUTHORS   Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B.,
            Kapatral,V., Bhattacharyya,A., Reznik,G., Mikhailova,N.,
            Lapidus,A., Chu,L., Mazur,M., Goltsman,E., Larsen,N., D'Souza,M.,
            Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M.,
            Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.
  TITLE     Genome sequence of Bacillus cereus and comparative analysis with
            Bacillus anthracis
  JOURNAL   Nature 423 (6935), 87-91 (2003)
  MEDLINE   22608415
   PUBMED   12721630
REFERENCE   2  (bases 1 to 304680)
  AUTHORS   Candelon,B., Gailloux,K., Ehrlich,D.S. and Sorokin,A.
  TITLE     The number of ribosomal RNA operons in Bacillus cereus
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 304680)
  AUTHORS   Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B.,
            Kapatral,V., Bhattacharyya,A., Reznik,G., Mikhailova,N.,
            Lapidus,A., Chu,L., Mazur,M., Goltsman,E., Larsen,N., D'Souza,M.,
            Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M.,
            Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de
            Vilvert, Jouy en Josas 78352, France
FEATURES            Location/Qualifiers
     source         1. .304680
                    /organism="Bacillus cereus ATCC 14579"
                    /mol_type="genomic DNA"
                    /strain="ATCC 14579"
                    /db_xref="ATCC:14579"
                    /db_xref="taxon:226900"
     gene           68. .427
                    /locus_tag="BC1239"
     CDS            68. .427
                    /locus_tag="BC1239"
                    /codon_start=1
                    /transl_table=11
                    /product="hypothetical Membrane Spanning Protein"
                    /protein_id="AAP08224.1"
                    /db_xref="GI:29894936"
                    /translation="MLRRKLLYLFLTVPLYAWLISMTKIELMALFLGYVFIFSNLNRI
                    QEQSILEICLFSISIELFSIVSIVLLNELFLRIHSFTLMKFWNIILQAICTYIVFVVL
                    KEIVGKQTVFQDNRKWE"
     gene           551. .2041
                    /locus_tag="BC1240"
     CDS            551. .2041
                    /locus_tag="BC1240"
                    /codon_start=1
                    /transl_table=11
                    /product="L-lactate permease"
                    /protein_id="AAP08225.1"
                    /db_xref="GI:29894937"
                    /translation="MLALIPIMMIFICLFLFKQTSLRSSLISYAVSVGIVLLSPTFQL
                    GISETVHATIKGWLICFIVGYVLFFGIFLFHLMNKMGYIDQVARFLEEVTQDRLLQML
                    LMCFGICPLIESVSGFGIGFMVAAPIFLSLGYKPFQAVLLSFIGLLASSWGAMATGTI
                    IGSQLINMPLTTLGTNTALLSIPMFAYFVILSLHVVGGWQAVIEKWKEGVGFFLLFSL
                    GIYLSNAYVSVELAGILSSIVTITFGFLIIKLKGKSGQNLITEHAAATEREVSIIKII
                    SPYIFLTVCILLSRLVPALHDLFRSYAVLDLKSYSYKLELLYSPGFWLGMTCLFTIIF
                    FRIPSNIIKQSLSQTIKQWIPFAITTTMFIAISELMGASGMHSLLAKTAGDTFGTFFV
                    FVAPFIGAIGGFLTGSNAGSNAMFIKLQMQTAQNVALPWQYVTTLQNTASSVATIACP
                    SRITLGAYLCNIPYRENELLKKTTLMIFGAVLLVVVEVIVWYMLRN"
     gene           2132. .2818
                    /locus_tag="BC1241"
     CDS            2132. .2818
                    /locus_tag="BC1241"
                    /codon_start=1
                    /transl_table=11
                    /product="hypothetical protein"
                    /protein_id="AAP08226.1"
                    /db_xref="GI:29894938"
                    /translation="MTLKNYGVLKGTVIQSEIGKGKTPHYQVHLQGETGVDYRIAINV
                    KSQSYPSEVLYFASNNIKSEAIHILPTLPFGFTEIKNNEPKVALDYIRGNLFDSNQMI
                    PLPPEKAGADNDLNEKIERYIKRAIEEKAIIYAFGERWGPEENTPDSYFHFKPGNGIH
                    DIHMNQGNVEKWQGDDGIWQDGGILIHFEKEEEWIGIFLAFQSQSWCTDEEGHARVPV
                    EHCDYKGNIK"
     gene           complement(2830. .3663)
                    /locus_tag="BC1242"
     CDS            complement(2830. .3663)
                    /locus_tag="BC1242"
                    /codon_start=1
                    /transl_table=11
                    /product="Integral membrane protein"
                    /protein_id="AAP08227.1"
                    /db_xref="GI:29894939"
                    /translation="MELVNSIFQILLTSVIQLLSLIGVIIVIGFLLGYLESLTRMYWS
                    RAFGRKGFLLTAWIGVPIHELGHAIMCVLFRHKIVATQFFPTDTSQGALGYVQHQYNQ
                    KSVYQRIGNFFIGIGPIISGITALILLMRYFVPESYFLFNTTLEKTIASTSINIEMIQ
                    NMLLSTFVLLKSLFTIGNLLNPSFWLFLFIAICISAHIALSKPDIKGSIDGVIVMFIV
                    LFLFNIITGLFQYDSNQLIGQVMKYNMYLIAFSSVALLFSCISTLVSFSFYKIRRGRS
                    F"
     gene           3860. .4630
                    /locus_tag="BC1243"
     CDS            3860. .4630
                    /locus_tag="BC1243"
                    /codon_start=1
                    /transl_table=11
                    /product="hypothetical protein"
                    /protein_id="AAP08228.1"
```

/db_xref="GI:29894940"
/translation="MKCPSCHTGNAAEAKFCGNCGHSLTEEVVASSGQEEGPEQAKEA
RPNETVEQAKRFASGYFQFFKHALQAPTAIMKSGAIEVRNGIVSLVLICFLGACIFYR
MMSAASAVTRTFAPDISTPTFFGESITVFFFLLLILTLFVGFIIFVSGKMMKSSFSFLE
VFGIWGTIATPTIVILVLSFLFSFLLIFFLPILLSVAATYIGISITVAVLKLDNGGLD
LVYTLIIANVLIGIATFMVLWSYISTIIQALTKGITGF"
gene 4650. .5885
/locus_tag="BC1244"
CDS 4650. .5885
/locus_tag="BC1244"
/codon_start=1
/transl_table=11
/product="IG hypothetical 16680"
/protein_id="AAP08229.1"
/db_xref="GI:29894941"
/translation="MNVCTKCGAQFEDGVQFCQNCGSKRGRPVVKKNMSGGTKVGITL
LALFVIVIIGLYLYGASYYTQVAQVDRMITILQERDGEKLAEIVTADDPSVMITRESL
TPLFSYIKENPSYVNELKGYLRQGEKQRDGIERVDFSLTKDGKYFFIFDRYKLKAKTY
YTTLLTNEKGVSLKMNGKEIDKTDDKKFEKQYGPFLPGNQVFQSDYKNDYVKLSREEK
VVLMKQSQYNVTIDLTLQGQYITVQTNAPGATLYVNQKPVTALAGEEITWGPVATDGS
ATIYLERNGESGRETTQVETITTLSSYNLPFQKKSTEKTVVYNVTPTPATGHVYNGFI
FPDSDIRKLTSADLTYLSKEQLKIARNEIYARHGHIFQTKDMQAYFAKQSWYRENPYF
KGTLTDIETYNIELIKSRE"
gene complement(5931. .6362)
/locus_tag="BC1245"
CDS complement(5931. .6362)
/locus_tag="BC1245"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAP08230.1"
/db_xref="GI:29894942"
/translation="MCAGLLAQLPDEPQEPKEPKPAVSLDQEFSINATIYSARAWLSN
DDTFAQDIWKATQFASASHAGKSIFPVGSVKIINFSDDTITVTASPESDHALKIVVPP
HSEAALTSGPLSHIQASTSGGSSKVTFLFHIFFSRDPGPAK"
gene 6560. .7894
/locus_tag="BC1246"
CDS 6560. .7894
/locus_tag="BC1246"
/EC_number="1.6.99.3"
/codon_start=1
/transl_table=11
/product="NADH dehydrogenase"
/protein_id="AAP08231.1"
/db_xref="GI:29894943"
/translation="MNYVIIGGDAAGMSATMQIVTNDENANVVTLEKGEIYSYAQCGL
PYVISGAIASTEKLIAHNVKTFRDKYGIDAKVRHEVTKVDTEKKMVYAEHTKTKDVFE
FPYDRLLIATGVRPVMPEWEGRELQGVHLLKTIPDAERILKTLETNKVEDVTIIGGGA
IGLEMAETFVELGKKVRMIERNDHIGTIYDADMAEYIHKEADKHHIEILTNENVKAFK
GNERVEAIETDKGTYKADLVLVSVGVKPNTDFLEGTNIRKNHKGAIEVNAYMQTNVQD
VYAAGDCATHYHVIKEIHDHIPLGTTANKQGRLAGLNMLDKRRAFKGTLGTGIIKFMD
LTLARTGLNEKEAKGLHIPYKTVKVDSTNMAGYYPNAKPLYLKLLYRSDTKQLLGGQV
IGEEGVDKRIDVIAMALFNKMSIHDLEDVDLSYAPPYNSVWDPIQQAARRAE"
gene 8055. .8465
/locus_tag="BC1247"
CDS 8055. .8465
/locus_tag="BC1247"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAP08232.1"
/db_xref="GI:29894944"
/translation="MAINMKTIEEWIAESNARHEEDFGHVVEEMKEVCVGLDNATLIY
TKNVFCFGKKVEVFFFFQDHVVIGQEKDEYVEIEKLKYDAITNSNLKTNDKNTTLELK
FANGQSINLDSLNDNYGTKNWLFARQIKSIFKLI"
gene complement(8496. .10037)
/locus_tag="BC1248"
CDS complement(8496. .10037)
/locus_tag="BC1248"
/EC_number="1.6.99.3"
/codon_start=1
/transl_table=11
/product="NADH oxidase (NOXASE)"
/protein_id="AAP08233.1"
/db_xref="GI:29894945"
/translation="MQLNTFLHHLHFSIDEIMPNHEVDWKDAPLPYKLYRNVPTIPLS
LEIPLSLSNSSTTPTLNEIGHYLWYSFGVTQLCQLNSGRNVLRRSIPSGGALYPNELY
IYLKIDDYPDGIYHYDAAHHRLILLREGNFDSYLADALGNRCNIHDCFGAAFVSTMFW
KNFFKYNNFSYRLQGLDSGVLIGQLLECAKQFGYTNGVYFQFLDRALNHLLGLSEGEE
SVYAVIPLSTEPETNWFHNDYHENKTVTSHELLQQIPPLAHEHFVRSKHVDEYPMITK
INEASMIESTAHFQTLAHEEHYQYHEHAVQLPKVERLSYDFLQLCRKRYSPDADFTLT
XWDAAELATLLQEASLSLPYSNDLDGKYINENARVSLYGCFYNVKDIKNGAYTYNSKT
HSIQPLRYGDLRYPLQSSMTMDNVNLFQVSLCLHVVGKKDYYTNALGYRGYRIHQMEA
GILVHKLVFAATAMGMGGHPLLSFDTNSCDQLYGIDAGNETSLIQVPVGAYRARNWLK
GALHN"
gene complement(10053. .11987)
/locus_tag="BC1249"
CDS complement(10053. .11987)
/locus_tag="BC1249"
/codon_start=1
/transl_table=11
/product="hypothetical Cytosolic Protein"
/protein_id="AAP08234.1"

Query Match 54.0%; Score 209; DB 1; Length 304680;
Best Local Similarity 71.4%; Pred. No. 2.1e-37;
Matches 275; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

```
Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              ||||||||     |    ||||||     || || | ||||  ||||||||  |  |||||
Db     244523 TCTTCTTCAATCTTTGGAAAATGTTGTGCAGCTTCGTCTAGTAAGTCACCTAACCCTAAT 244464

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              || ||||  ||||| || ||  | ||||| |||||||||||||| ||| || ||||| | |
Db     244463 CCGTGTGTACCTGAAATTGGGAATGGTTCGCCAAATCCTAATGCATAAAAGTCATAAATG 244404

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              ||  | |||||||||  ||| |||||||| || || || | ||| |||||||| || ||
Db     244403 TCACTGCGCATTTCCGGATTGTCTACTTTATTTACTGCAAGTACAACCGGTTTATTTGAA 244344

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
                |||||||||  || ||  ||||||  |  ||| |  || |||||  ||||   |
Db     244343 CGATATAAAATTTTTGCAACTTCTTCATCAGCTGCTGTTACACCGTCACGACCGTTTGTC 244284

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||| |||||||||||||||||| || || | ||| || ||    | |||||||||
Db     244283 ATAAAAATGATAACATCCGCTTCATCAATTGCTACTTCAGCTTGTTGACGAATTTGTGTC 244224

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              || ||  | || ||||| ||||| || || |||||||||| || || |||||  ||
Db     244223 AAAAACGGCTCGTCTCCAATATCAATTCCGCCCGTATCAATAATGTTAAATTCATGATTT 244164

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              |||||||| || |    ||||||||
Db     244163 AACCATTCTCCAGCGCTATAAATAC 244139
```

RESULT 10
AL596170
LOCUS AL596170 313450 bp DNA linear BCT 06-JUN-2002
DEFINITION Listeria innocua Clip11262 complete genome, segment 8/12.
ACCESSION AL596170 AL592022
VERSION AL596170.1 GI:16414292
KEYWORDS .
SOURCE Listeria innocua
ORGANISM Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Glaser,P., Frangeul,L., Buchrieser,C., Rusniok,C., Amend,A., Baquero,F., Berche,P., Bloecker,H., Brandt,P., Chakraborty,T., Charbit,A., Chetouani,F., Couve,E., de Daruvar,A., Dehoux,P., Domann,E., Dominguez-Bernal,G., Duchaud,E., Durant,L., Dussurget,O., Entian,K.D., Fsihi,H., Portillo,F.G., Garrido,P., Gautier,L., Goebel,W., Gomez-Lopez,N., Hain,T., Hauf,J., Jackson,D., Jones,L.M., Kaerst,U., Kreft,J., Kuhn,M., Kunst,F., Kurapkat,G., Madueno,E., Maitournam,A., Vicente,J.M., Ng,E.,

```
            Nedjari,H., Nordsiek,G., Novella,S., de Pablos,B., Perez-Diaz,J.C.,
            Purcell,R., Remmel,B., Rose,M., Schlueter,T., Simoes,N.,
            Tierrez,A., Vazquez-Boland,J.A., Voss,H., Wehland,J. and Cossart,P.
  TITLE     Comparative genomics of Listeria species
  JOURNAL   Science 294 (5543), 849-852 (2001)
  MEDLINE   21537279
   PUBMED   11679669
REFERENCE   2  (bases 1 to 313450)
  AUTHORS   Glaser,P., Frangeul,L. and Rusniok,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2001) Glaser P., Institut Pasteur, Genomique des
            Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
            Cedex 15, FRANCE
COMMENT     E-mail: pglaser@pasteur.fr
            Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
FEATURES             Location/Qualifiers
     source          1. .313450
                     /organism="Listeria innocua"
                     /mol_type="genomic DNA"
                     /strain="Clip11262"
                     /db_xref="taxon:1642"
     gene            complement(287. .1444)
                     /gene="lin1790"
     CDS             complement(287. .1444)
                     /gene="lin1790"
                     /note="similar to transmembrane transport proteins"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC97021.1"
                     /db_xref="GI:16414293"
                     /db_xref="SPTREMBL:Q92AX8"
                     /translation="MGAKGKFWILTMVVAISGLSQGVLLPLIAIILEEKGVSAGINGF
                     HATGIYLGVLLVSPFIEAPLHKYGYKPIILVGGGLVAIAIFAFPIWFNLYFWFILRLL
                     IGIGDHMLHFSSQTWIGAMSDPSKRGRNMAIYGLFFSVGFAIGPQLVNLAKVNANLPF
                     FLSGILVLIAWSLVWFIRNDFVGEKAVIRKISFWGSIKRFSGVFKMAWVAMIPPFLYG
                     ILETGLNATFPVVGLRDGLDTMMIAMIISSFSVGTIIFQVPIGIISDKFGRDKMLPLL
                     TGAGAVVFVLTAFVKIPIFFVIFFFILGILLGSLYSLGLSYMTDLTPLELLPAGNILV
                     GMFFSLGSIIGPSATGMMIGIFGNQIFYFVVAGILLLGCLLLALGGRKEAH"
     tRNA            complement(1508. .1579)
                     /product="tRNA-Glu"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 69.21"
     tRNA            complement(1585. .1675)
                     /product="tRNA-Ser"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 63.76"
     tRNA            complement(1712. .1784)
                     /product="tRNA-Asn"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 85.46"
     tRNA            complement(1791. .1864)
                     /product="tRNA-Ile"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 92.91"
     tRNA            complement(1891. .1961)
                     /product="tRNA-Gly"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 73.1"
     tRNA            complement(1984. .2056)
                     /product="tRNA-His"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 72.11"
     tRNA            complement(2083. .2155)
                     /product="tRNA-Phe"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 79.39"
     tRNA            complement(2160. .2235)
                     /product="tRNA-Asp"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 73.32"
     tRNA            complement(2240. .2313)
                     /product="tRNA-Met"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 78.6"
     tRNA            complement(2356. .2445)
                     /product="tRNA-Ser"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 66.89"
     tRNA            complement(2468. .2541)
                     /product="tRNA-Met"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 90.88"
     tRNA            complement(2553. .2626)
                     /product="tRNA-Met"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 77.07"
     tRNA            complement(2681. .2753)
                     /product="tRNA-Ala"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 84.64"
     tRNA            complement(2773. .2846)
                     /product="tRNA-Pro"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 86.85"
     tRNA            complement(2857. .2930)
                     /product="tRNA-Arg"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 74.21"
     tRNA            complement(2940. .3025)
                     /product="tRNA-Leu"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 66.88"
     tRNA            complement(3040. .3114)
                     /product="tRNA-Gly"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 87.88"
     tRNA            complement(3130. .3211)
                     /product="tRNA-Leu"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 69.82"
     tRNA            complement(3217. .3289)
                     /product="tRNA-Lys"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 88.37"
     tRNA            complement(3330. .3405)
                     /product="tRNA-Thr"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 95.38"
     tRNA            complement(3414. .3486)
                     /product="tRNA-Val"
                     /note="tRNAscan-SE vs 1.3 result - Cove score = 86.53"
     gene            complement(3503. .3612)
                     /gene="rRNA-5s"
     rRNA            complement(3503. .3612)
                     /gene="rRNA-5s"
     gene            complement(3693. .6623)
                     /gene="rRNA-23s"
     rRNA            complement(3693. .6623)
                     /gene="rRNA-23s"
     gene            complement(6869. .8423)
                     /gene="rRNA-16s"
     rRNA            complement(6869. .8423)
                     /gene="rRNA-16s"
     gene            complement(8850. .9335)
                     /gene="lin1791"
     terminator      complement(8850. .8868)
                     /gene="lin1791"
     CDS             complement(8876. .9322)
                     /gene="lin1791"
                     /note="similar to transcription regulators (Fur family),
                     PerR in B. subtilis"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC97022.1"
                     /db_xref="GI:16414294"
                     /db_xref="SPTREMBL:Q92AX7"
                     /translation="MAVSNATLKEAVDVLKKTGVRITPQRHAILEFLINSHTHPTADD
                     IYRSLEGNFPNMSVATVYNNLRVFRDAGLIKELSYGDASSRFDFSTSNHYHAICNVCG
                     KIVDFHYPGLDEVEHFAAHVTGYEIDNHRLEVYGTCPECKEKQSNN"
     RBS             complement(9330. .9335)
                     /gene="lin1791"
     gene            complement(9405. .10361)
                     /gene="lin1792"
     CDS             complement(9405. .10346)
                     /gene="lin1792"
                     /note="similar to glycerate dehydrogenases"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC97023.1"
                     /db_xref="GI:16414295"
                     /db_xref="SPTREMBL:Q92AX6"
                     /translation="MKVLFTLDVPERLKNLQAEKFPDDTFYFESIDHFTNLGEVDVII
                     TYGSNITEEKIKKATNLKLIMVFSAGVDSLPTKIIQEQKIKVANVRGIHAIPMGEYAL
                     SFMLSHVKKAAFFYKMQKEEKWASEEPITELAGKTLVVAGTGAIGAKVAEFAQAFDME
                     VIGINTTGHPVKPFSKTYAMTDLEKVAPLADFFVSVLPQTEETSGIYQLSFFEKMKTN
                     AVFINIGRGSAVELETLERASKEEQIAHFYLDVLPEEPLPAESYLWQASNVTITPHVS
```

```
                     GHSDKYLDRSFEIWFENINHLKENTKLRNEIDLNKGY"
     RBS             complement(10356. .10361)
                     /gene="lin1792"
     gene            10476. .11787
                     /gene="gsaB"
     RBS             10476. .10481
                     /gene="gsaB"
     CDS             10489. .11787
                     /gene="gsaB"
                     /codon_start=1
                     /transl_table=11
                     /product="glutamate-1-semialdehyde aminotransferase"
                     /protein_id="CAC97024.1"
                     /db_xref="GI:16414296"
                     /db_xref="SPTREMBL:Q92AX5"
                     /translation="MDHSMSKKLHDEALLHIVGGVNSPSRSNKGVGGGIPVTMERANG
                     AYFYDVDGNKYIDYLAAFGPIITGHAHPHITEAITKAAQNGVLYGTPTKHEITFAKML
                     KEAIPSLEKVRFTNSGTEAVMTTIRVARAYTGRDKIIKFAGCYHGHFDLVLVEAGSGP
                     STLGIPDSAGVTRSTAEEVITVPFNDLTSFKEALAVWGDQVAAVLVEPIVGNFGMVAP
                     AEGFLEAVNELAHENGSLVIYDEVITAFRFMYGGAQNYLGVIPDLTAMGKIIGGGLPI
                     GAYGGRVDIMEKVAPLGPAYQAGTHAGNPASILSGIACLEVLQEEGLYDRFEKYGSML
                     KEGIEKAAIKHGIAVTVNQIVGALTVYFTDEPVTNYAEAGATNGDLFGRFFKGMLEEG
                     INLAPSKYEAWFITSAHSEADILETIQAVDTVFGKLVQGK"
     gene            join(11879. .12981,12990. .13016)
                     /gene="lin1794"
     RBS             11879. .11884
                     /gene="lin1794"
     CDS             11893. .12981
                     /gene="lin1794"
                     /note="similar to hypothetical proteins"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC97025.1"
                     /db_xref="GI:16414297"
                     /db_xref="SPTREMBL:Q92AX4"
                     /translation="MKFGARILKTGIAITLALFIAQLCNSPSPSLAGISAVFAIQPSI
                     YRSYRTILERAQGNVIGAIIAIIFGLYIGNDFILIGVASIICVALLMQFRLENTIGLA
```

Query Match 53.2%; Score 205.8; DB 1; Length 313450;
Best Local Similarity 70.9%; Pred. No. 1.1e-36;
Matches 273; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| ||||    |||||||| |  ||| ||||| | ||  |||||||| ||||
Db     276305 TCCTCTTCTTCTTTTGGAAAATGAGCACGAACAGCATCAAGCATATCACCAAGCCCTAGT 276364

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              ||||| || || || || |||||||| |||||||| || |  ||||| || ||||| |
Db     276365 CCATGAGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATC 276424

Qy         123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
               |    |||||||||    |||||||||| |||| |||||| || |  ||||| |||||
Db     276425 TGATCACGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 276484

Qy         183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
                 ||| | |||||  || ||   ||| ||    |  || |  |||||||| | ||
Db     276485 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACCCCTTCACGACCATTGGTA 276544

Qy         243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
               |||||||||||| || || |||||||| || |||||||| || || || | ||||||   |
Db     276545 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 276604

Qy         303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
               |||||||  | ||   ||  |||||||||||||||||||||||| || || || | |
Db     276605 AAGAATGGTTCGTCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 276664

Qy         363 AACCATTCACCTGAAGAATAAATAC 387
               | ||||||  |||||  ||| || |
Db     276665 AGCCATTCCGCTGAATTATATATGC 276689
```

RESULT 11
AX413016/c

```
LOCUS       AX413016              319630 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 7 from Patent WO0228891.
ACCESSION   AX413016
VERSION     AX413016.1  GI:21445474
KEYWORDS    .
SOURCE      Listeria innocua
  ORGANISM  Listeria innocua
            Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE   1
  AUTHORS   Kunst,F. and Glaser,P.
  TITLE     Listeria inocua, genome and applications
  JOURNAL   Patent: WO 0228891-A 7 11-APR-2002;
            INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
            SCIENTIFIQUE (CNRS) (FR)
FEATURES             Location/Qualifiers
     source          1. .319630
                     /organism="Listeria innocua"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1642"
BASE COUNT   105207 a  55428 c  66726 g  92263 t      6 others
ORIGIN
```

Query Match 53.2%; Score 205.8; DB 6; Length 319630;
Best Local Similarity 70.9%; Pred. No. 1.1e-36;
Matches 273; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| ||||    |||||||| |  ||| ||||| | ||  |||||||| ||||
Db      51123 TCCTCTTCTTCTTTTGGAAAATGAGCACGAACAGCATCAAGCATATCACCAAGCCCTAGT 51064

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              ||||| || || || || |||||||| |||||||| || |  ||||| || ||||| |
Db      51063 CCATGAGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATC 51004

Qy         123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
               |    |||||||||    |||||||||| |||| |||||| || |  ||||| |||||
Db      51003 TGATCACGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 50944

Qy         183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
                 ||| | |||||  || ||   ||| ||    |  || |  |||||||| | ||
Db      50943 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACCCCTTCACGACCATTGGTA 50884

Qy         243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
               |||||||||||| || || |||||||| || |||||||| || || || | ||||||   |
Db      50883 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 50824

Qy         303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
               |||||||  | ||   ||  |||||||||||||||||||||||| || || || | |
Db      50823 AAGAATGGTTCGTCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 50764

Qy         363 AACCATTCACCTGAAGAATAAATAC 387
               | ||||||  |||||  ||| || |
Db      50763 AGCCATTCCGCTGAATTATATATGC 50739
```

```
RESULT 12
AL591981
LOCUS       AL591981              347050 bp    DNA     linear   BCT 06-JUN-2002
DEFINITION  Listeria monocytogenes strain EGD, complete genome, segment 9/12.
ACCESSION   AL591981 AL591824
VERSION     AL591981.1  GI:16411141
KEYWORDS    .
SOURCE      Listeria monocytogenes
  ORGANISM  Listeria monocytogenes
            Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE   1
  AUTHORS   Glaser,P., Frangeul,L., Buchrieser,C., Rusniok,C., Amend,A.,
            Baquero,F., Berche,P., Bloecker,H., Brandt,P., Chakraborty,T.,
            Charbit,A., Chetouani,F., Couve,E., de Daruvar,A., Dehoux,P.,
            Domann,E., Dominguez-Bernal,G., Duchaud,E., Durant,L.,
            Dussurget,O., Entian,K.D., Fsihi,H., Portillo,F.G., Garrido,P.,
            Gautier,L., Goebel,W., Gomez-Lopez,N., Hain,T., Hauf,J.,
            Jackson,D., Jones,L.M., Kaerst,U., Kreft,J., Kuhn,M., Kunst,F.,
```

```
            Kurapkat,G., Madueno,E., Maitournam,A., Vicente,J.M., Ng,E.,
            Nedjari,H., Nordsiek,G., Novella,S., de Pablos,B., Perez-Diaz,J.C.,
            Purcell,R., Remmel,B., Rose,M., Schlueter,T., Simoes,N.,
            Tierrez,A., Vazquez-Boland,J.A., Voss,H., Wehland,J. and Cossart,P.
  TITLE     Comparative genomics of Listeria species
  JOURNAL   Science 294 (5543), 849-852 (2001)
  MEDLINE   21537279
   PUBMED   11679669
REFERENCE   2  (bases 1 to 347050)
  AUTHORS   Glaser,P., Frangeul,L. and Rusniok,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des
            Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
            Cedex 15, FRANCE
COMMENT     E-mail: pglaser@pasteur.fr
            Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
FEATURES             Location/Qualifiers
     source          1. .347050
                     /organism="Listeria monocytogenes"
                     /mol_type="genomic DNA"
                     /strain="EGD-e"
                     /db_xref="taxon:1639"
     gene            complement(95. .841)
                     /gene="lmo1688"
     CDS             complement(95. .841)
                     /gene="lmo1688"
                     /note="similar to glucose 1-dehydrogenase"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99766.1"
                     /db_xref="GI:16411142"
                     /db_xref="SPTREMBL:Q8Y6J6"
                     /translation="MNKVALVTGSSRGLGREIAIALAKEGYDIAVNFSRNRKKAEEVQ
                     QEIEQLGRKCVIFKANVGDVEKVRELFKAVDEEFGRLDIFINNAASGVLRPLMELEES
                     HWDWTMNINAKALLFAGQEAAKLMQRHQSGKIISLSSIGSIRYLENYTTVGVSKAAVE
                     SLTRYLAVELAPFGIAVNAVSGGLIETDALNHFPNREELLKDAVSKTPAGRMIEPNDL
                     VNAVLFLASEKADMIRGQTILVDGGRTLLV"
     gene            complement(join(845. .1942,1948. .1953))
                     /gene="lmo1689"
     CDS             complement(845. .1942)
                     /gene="lmo1689"
                     /note="similar to A/G-specific adenine glycosylase"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99767.1"
                     /db_xref="GI:16411143"
                     /db_xref="SPTREMBL:Q8Y6J5"
                     /translation="MRKMKRLTWDETKITAFQEALVSWYEANKRVLPWRENTEPYRIW
                     VSEIMLQQTKVDTVIPYFNRFMTQFPTMESFVNADEADILKAWEGLGYYSRVRNLQTA
                     MKQVMADFSGEVPTDLTTILSLKGVGPYTAGAILSIAYNQAEPAVDGNVMRVIARVLE
                     IGEDIMKASTRKIFEEVLYQLIDKKNPAAFNQGLMEIGALVCTPTKPMCMLCPLQPFC
                     EAHKNGVETNYPVKIKKVKMKTKELLSIIVISEDGKIAIEKRPENGLLANMWQFPTIE
                     ISKKENDEVAKLQFLHNYGLEVLLEDEPIAHIKHVFSHLVWKMDIRVAKLQSAIPNEN
                     WYFATEEEMKRLAFPVPYQKMWQAWKDFKGE"
     gene            complement(850. .855)
                     /gene="lmo1688"
     RBS             complement(850. .855)
                     /gene="lmo1688"
     RBS             complement(1948. .1953)
                     /gene="lmo1689"
     gene            join(2129. .3123,3130. .3147)
                     /gene="lmo1690"
     RBS             2129. .2134
                     /gene="lmo1690"
     CDS             2143. .3123
                     /gene="lmo1690"
                     /note="similar to hypothetical proteins"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99768.1"
                     /db_xref="GI:16411144"
                     /db_xref="SPTREMBL:Q8Y6J4"
                     /translation="MDTGTHVVMGIALGALATVDPVVAGSSQAAIGIMTATIIGSQIP
                     DIDTVLKLKNNADYIRNHRGITHSLPMLAIWPLLISSILYLLFPAATFIHLLLWTFIA
                     VGLHIFVDIFNAYGTQAVRPFKETWVAFGFINTFDWFIFGSHVVAIAAWLLGSPVLPT
                     FVTLYVILALYYVARFVTQRMIKHAVQNLIPDSEEIIIASTIHFFQWRVAVTTKDHYY
                     VGRAFKRNISIYEKFDRLPVPDNEIIRSAKKDKNLAAFISFSKVYNWRIEEKLDGTYV
                     TFTDLRYRSNGHYPFVAVVKLDDDLKIVSSYTGWIFSTEKLYKKLAPVSI"
     gene            complement(join(3130. .3147,3156. .3617,3625. .3630))
                     /gene="lmo1691"
     terminator      3130. .3147
                     /gene="lmo1690"
     terminator      complement(3130. .3147)
                     /gene="lmo1691"
     CDS             complement(3156. .3617)
                     /gene="lmo1691"
                     /note="similar to deoxyuridine triphosphate
                     nucleotidohydrolases"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99769.1"
                     /db_xref="GI:16411145"
                     /db_xref="SPTREMBL:Q8Y6J3"
                     /translation="MKVRGFEVVNEASRKFPEQTISLPIRGDKGSAGYDFFSNETVTI
                     VPGEKHIFWTDIKSYMQEDEVLNIYVRSSIGIKKGLLLCNGTGIIDSSYYSNPGNDGN
                     IGIAIKNFSNEPVSIEAGERVAQGVFQKYLVADTDIVANESRVGGVGSTGR"
     RBS             complement(3625. .3630)
                     /gene="lmo1691"
     gene            complement(3629. .3862)
                     /gene="lmo1692"
     CDS             complement(3629. .3862)
                     /gene="lmo1692"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99770.1"
                     /db_xref="GI:16411146"
                     /db_xref="SPTREMBL:Q8Y6J2"
                     /translation="MYTYLDELTAELMVKNPHLDKEQALWWIEMLWSDFESSYAKAGY
                     PYRGPEYAADYVRQQIERHGSFLHQVERKDPNK"
     gene            complement(join(3864. .4673,4680. .4685))
                     /gene="lmo1693"
     CDS             complement(3864. .4673)
                     /gene="lmo1693"
                     /note="similar to hypothetical proteins"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99771.1"
                     /db_xref="GI:16411147"
                     /db_xref="SPTREMBL:Q8Y6J1"
                     /translation="MKITSISVQQKNKERYNIFIDEKYNFSVDEEVLARYQLMKGKVL
                     TEADIEEIKQADMVRKGLNKAINFLSHRVRSEKEIRDYLRKQEMEPFAIDEILKKLAN
                     MDYINDFEFAELYTKTQIKTTLKGPRTIERELVEKGLTREIISRVIEEYSDEAQLENA
                     TKQAMKIMKRNNKSAKKMLQQKIITDLIQKGFTSELAKAAATEATSELDVADEAEILQ
                     KQIEKTMRKNKRYKPSIAKQKTITSLMQKGFSYDTIQSYLTENEISFEEEE"
     gene            complement(3872. .3877)
                     /gene="lmo1692"
     RBS             complement(3872. .3877)
                     /gene="lmo1692"
     RBS             complement(4680. .4685)
                     /gene="lmo1693"
     gene            join(4757. .5673,5681. .5708)
                     /gene="lmo1694"
     RBS             4757. .4762
                     /gene="lmo1694"
     CDS             4771. .5673
                     /gene="lmo1694"
                     /note="similar to CDP-abequose synthase"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99772.1"
                     /db_xref="GI:16411148"
                     /db_xref="SPTREMBL:Q8Y6J0"
                     /translation="MHILLTGATGFIGDHLVHELEKSDHELYILTRQKLKNRANVHYI
                     EWLNEDKLPNLEDLPVDVCINLAGAGLMDEKWTYDRKKVIVNSRIEATSALLSIVKKM
                     KSKPKLWINASAIGAYTSSKSTIYLDTEENTYADNFLGKTVYEWEKTASAASDLGIRV
                     VYARFGLVLGTNGGSFPVFEKLFQTYTGGRFGNGRQWYSWIHVDDVVAAILFIFDHEQ
```

```
                     INGVVNFTAPHPVQEKKFAERLGKKMHKPYKTPVPKKIIKFILGERAMTILDSQRAYP
                     EXLMSNHFEFRFETLQEALDDLLD"
     terminator      5681. .5708
                     /gene="lmo1694"
     gene            complement(join(5682. .8291,8299. .8304))
                     /gene="lmo1695"
     terminator      complement(5682. .5709)
                     /gene="lmo1695"
     CDS             complement(5694. .8291)
                     /gene="lmo1695"
                     /note="similar to putative membrane proteins"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC99773.1"
                     /db_xref="GI:16411149"
                     /db_xref="SPTREMBL:Q8Y6I9"
                     /translation="MKEKLMQAYAWFQKNSTVVKIVFITFVMAFVIFEIINIATGIDY
                     PSLKENLTSQSPEQIFIMFIVGLIAVTPMLLYDYVIVKLLPGKFSPSHVIASGWITNT
                     FTNIGGFGGVLGASLRASFYGKNASHKEILLAISKIALFLVSGLSIYCLVSLATLLIP
                     GFADHFVNYWPWLLAGGLYFPILFTITKWKSKSLFVDLPIKRELTLIIASLLEWGFAF
                     GCFAIIGTLMGEPVDIFKVFPLFVIASVIGIASMVPGGVGTFDVVMILGLSQLGVSQE
                     LALAWNLFYRIFYYIIPFVVGLLFFVQKAGKKVNDFLEGLPLLFLQKVAHRFLVIFVY
                     GSGLLLILSSAVPNAIYHVPFLYKIMPFNFLFTSQITIVAFGFLLLGLARGIECKTKK
                     AYIITVIVLGCAIFNTLARVFSMKQAIFLGIVLLCLFLARNEFYREKLVYTWSKVIID
                     SIIFIVCLAGYIVIGIYNSPNIKHSKEIPDYLRIASEHLWLVGFVGVFIAVVSLVIIY
                     IYLSTTKEKLGSPFEAVKVREHLAKWGGNEVSHTMFLRDKLLFWAAEGEVLFSYRIIA
                     DKMVIMGEPTGNMDKMEAAIEEVMMNADRFGYRPVFYEVRGTMIPYLHDHGFDFIKLG
                     EEGFVDVQNFTMSGKKKKGERALMNKLEREGYTFEIIEPPFNHDTWTTLRAVSDEWLD
                     GREEKGFSLGFFDTYYLEQAPIAIAKNGEGTIVGFASMMPSYTDEMTSIDLMRYSKEA
                     PSGIMDFLFINLFEKAKEDGFQTFNAGMAPLANVGESKYAFLGERLAGLVYRYSQGFY
                     GFKGLRNFKSKYVTEWEQKFVAFRKRSSIAFTMLQLMILVGKKRPLANSQVVLDFPLE
                     EETKKPDSE"
     RBS             complement(8299. .8304)
                     /gene="lmo1695"
     gene            complement(8318. .9007)
                     /gene="lmo1696"
     CDS             complement(8318. .8992)
                     /gene="lmo1696"

  Query Match             53.2%;  Score 205.8;  DB 1;  Length 347050;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-36;
  Matches  273;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| ||||    ||||||||    ||| |||||  | ||  ||| |||| |||| 
Db     258933 TCCTCTTCTTCTTTTGGAAAATGAGCGCGAACAGCATCAAGCATGTCGCCAAGCCCTAGT 258992

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              |||||||| || || || |||||||| |||||||| || |  ||||| || ||||| | 
Db     258993 CCATGTGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATT 259052

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              |     ||||||||    |||||||||| |||| |||||| || |  ||||| ||||| 
Db     259053 TGATCTCGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 259112

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
              ||| | |||||  || ||   ||| ||    |  || | |||||||||  | ||
Db     259113 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACTCCTTCACGACCATTGGTA 259172

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||||| || || |||||||| || |||||||| || || || | ||||||   |
Db     259173 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 259232

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              ||||||| |||    || ||||||||||||||||||| || || || | | |
Db     259233 AAAAATGGTTCATCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 259292

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              | ||||||  |||||  ||| || |
Db     259293 AGCCATTCCGCTGAATTATATATGC 259317


RESULT 13
AX417046
LOCUS       AX417046               349980 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 4037 from Patent WO0228891.
ACCESSION   AX417046
VERSION     AX417046.1  GI:21449656
KEYWORDS    .
SOURCE      Listeria innocua
  ORGANISM  Listeria innocua
            Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE   1
  AUTHORS   Kunst,F. and Glaser,P.
  TITLE     Listeria inocua, genome and applications
  JOURNAL   Patent: WO 0228891-A 4037 11-APR-2002;
            INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
            SCIENTIFIQUE (CNRS) (FR)
FEATURES             Location/Qualifiers
     source          1. .349980
                     /organism="Listeria innocua"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1642"
                     /note="seq 2058, original length: 3.011.208 replaced
                     by-seq 2058: 0.000.001 to 0.349.980-seq 4032: 0.300.001 to
                     0.649.980-seq 4033: 0.600.001 to 0.949.980-seq 4034:
                     0.900.001 to 1.249.980-seq 4035: 1.200.001 to
                     1.549.980-seq 4036: 1.500.001 to 1.849.980-seq 4037:
                     1.800.001 to 2.149.980-seq 4038: 2.100.001 to
                     2.449.980-seq 4039: 2.400.001 to 2.749.980-seq 4040:
                     2.700.001 to 3.049.980-seq 4041: 3.000.001 to 3.011.208"
BASE COUNT   101055 a  72969 c  60688 g 115268 t
ORIGIN

  Query Match             53.2%;  Score 205.8;  DB 6;  Length 349980;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-36;
  Matches  273;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| ||||    ||||||||    ||| |||||  | ||  ||| |||| |||| 
Db     266305 TCCTCTTCTTCTTTTGGAAAATGAGCACGAACAGCATCAAGCATATCACCAAGCCCTAGT 266364

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              |||||| || || || || |||||||| |||||||| || |  ||||| || ||||| | 
Db     266365 CCATGAGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATC 266424

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              |     ||||||||||    |||||||||| |||| |||||| || |  ||||| ||||| 
Db     266425 TGATCACGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 266484

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
              ||| | |||||  || ||   ||| ||    |  || | |||||||||  | ||
Db     266485 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACCCCTTCACGACCATTGGTA 266544

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||||| || || |||||||| || |||||||| || || || | ||||||   |
Db     266545 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 266604

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              ||||||| |||    || ||||||||||||||||||| || || || | | |
Db     266605 AAGAATGGTTCGTCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 266664

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              | ||||||  |||||  ||| || |
Db     266665 AGCCATTCCGCTGAATTATATATGC 266689


RESULT 14
AX641670
LOCUS       AX641670               349980 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2860 from Patent WO0101118.
ACCESSION   AX641670
VERSION     AX641670.1  GI:28474431
KEYWORDS    .
SOURCE      Listeria monocytogenes
  ORGANISM  Listeria monocytogenes
```

```
            Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE   1
  AUTHORS   Buchrieser,C., Frangeul,L., Couve,E., Rusniok,C., Fsihi,H.,
            Dehoux,P., Dussurget,O., Chetouani,F., Nedjari,H., Glaser,P.,
            Kunst,F., Cossart,P., Daniels,J., Goebel,W., Kreft,J., Kuhn,M.,
            Ng,E., Vasquez-Boland,J., Dominguez-Bernal,G., Garrido-Garcia,P.,
            Tierrez-Martinez,A., Amend,A., Chakraborty,T., Domann,E., Hain,T.,
            Berche,P., Charbit,A., Durant,L., Perez-Diaz,J.C., Baquero,F.,
            garcia del Portillo,F., Gomez-Lopez,N., Maduenio,E., de Pablos,B.,
            Wehland,J., Kaerst,U., Entian,K.D., Hauf,J., Rose,M. and Voss,H.
  TITLE     Listeria monocytogenes genome, polypeptides and uses
  JOURNAL   Patent: WO 0101118-A 2860 11-APR-2001;
            INSTITUT PASTEUR (FR)
FEATURES             Location/Qualifiers
     source          1. .349980
                     /organism="Listeria monocytogenes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1639"
                     /note="Seq 1 for big: original length: 2944528-splitted
                     into 10 <223>seq 0001 : From 0.000.001 to 0.349.980
                     length: 349.980 <223>seq 2855 : From 0.300.001 to
                     0.649.980 length: 349.980 <223>seq 2856 : From 0.600.001
                     to 0.949.980 length: 349.980 <223>seq 2857 : From
                     0.900.001 to 1.249.980 length: 349.980 <223>seq 2858 :
                     From 1.200.001 to 1.549.980 length: 349.980 <223>seq 2859
                     : From 1.500.001 to 1.849.980 length: 349.980 <223>seq
                     2860 : From 1.800.001 to 2.149.980 length: 349.980
                     <223>seq 2861 : From 2.100.001 to 2.449.980 length:
                     349.980 <223>seq 2862 : From 2.400.001 to 2.749.980
                     length: 349.980 <223>seq 2863 : From 2.700.001 to
                     2.944.528 length: 244.528"
BASE COUNT    99761 a  75437 c  61177 g 113605 t
ORIGIN

  Query Match             53.2%;  Score 205.8;  DB 6;  Length 349980;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-36;
  Matches  273;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy          3 TCTTCTTCCTCTTCACCAAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAA 62
              || ||||| ||||    ||||||||    ||| ||||| | || ||| ||||| ||||
Db     211933 TCCTCTTCTTCTTTTGGAAAATGAGCGCGAACAGCATCAAGCATGTCGCCAAGCCCTAGT 211992

Qy         63 CCATGTGACCCTGATATCGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACG 122
              |||||||| || || || |||||||| |||||||| || |  ||||| || ||||| |
Db     211993 CCATGTGAACCAGAAATTGGATACGGCTCACCAAACCCAAGAGAATAAAAGTCATAAATT 212052

Qy        123 TCTGTACGCATTTCCATATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGAT 182
              |     ||||||||    |||||||||||| |||| |||||| || |  ||||| |||||
Db     212053 TGATCTCGCATTTCTGGGTTATCTACTTTATTAATCGCTAAAACAATTGGTTTATTAGAC 212112

Qy        183 TTGTATAAAATTTGAGCGACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACC 242
              ||| | |||||  || ||   ||| ||    |  || | |||||||||  | ||
Db     212113 CGGTAAAGAATTTTTGCTACTTGTTCGTCTGCATCGGTAACTCCTTCACGACCATTGGTA 212172

Qy        243 ATAAAAATAATAACATCCGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTT 302
              |||||||||||| || || |||||||| || |||||||| || || || | ||||||   |
Db     212173 ATAAAAATAATTACGTCTGCTTCATCAATTGCGATTTCCGCTTGTGCGCGAATTTGCTCT 212232

Qy        303 TGGAATGGTGCATCACCAATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTT 362
              ||||||  ||||'  ||  ||||||||||||||||||||| || || || | |
Db     212233 AAAAATGGTTCATCGGAAAGATCAATACCACCTGTATCAATAATGTTAAATTCTTTTCCA 212292

Qy        363 AACCATTCACCTGAAGAATAAATAC 387
              | ||||||  |||||  ||| || |
Db     212293 AGCCATTCCGCTGAATTATATATGC 212317


RESULT 15
BACSERA/c
LOCUS       BACSERA                24887 bp    DNA     linear   BCT 09-DEC-1998
DEFINITION  Bacillus subtilis phosphoglycerate dehydrogenase (serA), ypaA,
            ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG, ypbH,
            glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortex
            lytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphate
            kinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+ dependent
            glycerol-3-phosphate dehydrogenase (glyc), yphE and yphF genes,
            complete cds.
ACCESSION   L47648
VERSION     L47648.1  GI:1146195
KEYWORDS    .
SOURCE      Bacillus subtilis
  ORGANISM  Bacillus subtilis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1  (bases 24112 to 24887)
  AUTHORS   Roels,S., Driks,A. and Losick,R.
  TITLE     Characterization of spoIVA, a sporulation gene involved in coat
            morphogenesis in Bacillus subtilis
  JOURNAL   J. Bacteriol. 174 (2), 575-585 (1992)
  MEDLINE   92105027
   PUBMED   1729246
REFERENCE   2  (bases 1 to 24887)
  AUTHORS   Sorokin,A., Zumstein,E., Azevedo,V., Ehrlich,S.D. and Serror,P.
  TITLE     The organization of the Bacillus subtilis 168 chromosome region
            between the spoVA and serA genetic loci, based on sequence data
  JOURNAL   Mol. Microbiol. 10 (2), 385-395 (1993)
  MEDLINE   95020538
   PUBMED   7934829
REFERENCE   3  (bases 1 to 24887)
  AUTHORS   Sorokin,A., Azevedo,V., Zumstein,E., Galleron,N., Ehrlich,S.D. and
            Serror,P.
  TITLE     Sequence analysis of the Bacillus subtilis chromosome region
            between the serA and kdg loci cloned in a yeast artificial
            chromosome
  JOURNAL   Microbiology 142 (Pt 8), 2005-2016 (1996)
  MEDLINE   96349105
   PUBMED   8760912
FEATURES             Location/Qualifiers
     source          1. .24887
                     /organism="Bacillus subtilis"
                     /mol_type="genomic DNA"
                     /strain="Marburg"
                     /sub_strain="168"
                     /db_xref="taxon:1423"
     terminator      complement(1. .41)
                     /citation=[2]
                     /citation=[3]
                     /evidence=experimental
     gene            complement(40. .1617)
                     /gene="serA"
     CDS             complement(40. .1617)
                     /gene="serA"
                     /function="serine biosynthesis"
                     /citation=[2]
                     /citation=[3]
                     /codon_start=1
                     /evidence=experimental
                     /transl_table=11
                     /product="phosphoglycerate dehydrogenase"
                     /protein_id="AAC83943.1"
                     /db_xref="GI:1146196"
                     /translation="MFRVLVSDKMSNDGLQPLIESDFIEIVQKNVADAEDELHTFDAL
                     LVRSATKVTEDLFNKMTSLKIVGRAGVGVDNIDIDEATKHGVIVINAPNGNTISTAEH
                     TFAMISSLMRHIPQANISVKSREWNRTAYVGSELYGKTLGIVGLGRIGSEIAQRRGAF
                     GMTVHVFDPFLTEERAKKIGVNSRTFEEVLESADIITVHTPLTKETKGLLNKETIAKT
                     KKGVRLINCARGGIIDEAALLEALENGHVAGAALDVFEVEPPVDNKLVDHPLVIATPH
                     LGASTKEAQLNVAAQVSEEVLQFAKGLPVMSAINLPAMTKDEFAKIKPYHQIAGKIGS
                     LVSQCMKEPVQDVAIQYEGTIAKLETSFITKALLSGFLKPRVDSTVNEVNAGGVAKER
                     GISFSEKISSSESGYDNCISVKVTGDRSTFTVTATYIPHFGERIVEINGFNIDFYPTG
                     HLVYIQHQDTTGVIGRVGRILGDNDINIATMQVGRKEKGGEAIMMLSFDRHLEDKIVK
                     ELTNVPDIVSVKLIDLP"
     gene            2114. .2686
                     /gene="ypaA"
     CDS             2114. .2686
                     /gene="ypaA"
                     /note="putative"
                     /citation=[3]
```

```
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAC83944.1"
                     /db_xref="GI:1146197"
                     /translation="MKVKKLVVVSMLSSIAFVLMLLNFPFPGLPDYLKIDFSDVPAII
                     AILIYGPLAGIAVEAIKNVLQYIIQGSMAGVPVGQVANFIAGTLFILPTAFLFKKLNS
                     AKGLAVSLLLGTAAMTILMSILNYVLILPAYTWFLHSPALSDSALKTAVVAGILPFNM
                     IKGIVITVVFSLIFIKLKPWIEQQRSAHIH"
terminator           2686. .2721
                     /note="putative"
                     /citation=[3]
gene                 complement(2726. .2974)
                     /gene="fer"
CDS                  complement(2726. .2974)
                     /gene="fer"
                     /note="ypbA; similar to B.stearothermophilus ferredoxin;
                     putative"
                     /citation=[3]
                     /codon_start=1
                     /transl_table=11
                     /product="ferredoxin"
                     /protein_id="AAC83945.1"
                     /db_xref="GI:1146198"
                     /translation="MAKYTIVDKDTCIACGACGAAAPDIYDYDDEGIAFVTLDENKGV
                     VEVPEVLEEDMIDAFEGCPTDSIKVADEPFEGDPLKFE"
gene                 3240. .4298
                     /gene="ypbB"
CDS                  3240. .4298
                     /gene="ypbB"
                     /note="putative"
                     /citation=[3]
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAC83946.1"
                     /db_xref="GI:1146199"
                     /translation="MSLNYFDIMVLDCLCKINGERSGSAVFHLFKGKRSSQTIQDAGL
                     FQTAKYFGMAAKCSRSDISASLDKLEKHSYLAPMSESDTYKVTASGAAVLRHALSERP
                     WPVHCHGAHYQQAAGVLWKRLSLLVQVLSHKQQGSRQYIPVTKDHKTLHWVKKYLSRH
                     TDHIEMAKSLFAMLEAHLKKIENKAAQIFVYSLTSHHRIGYTSRQLADTLKEDEWYVY
                     IMFWASVHYFIHSLPECEDALLKDLLSDVHLDNALTESTRKTWQMVKQGFPIQRIAEI
                     RKLKTATIEDHIVEISLHEPAFMINDYVSAEDQLQIAEFAKRMRTNKIKQIRDGLEQR
                     FSYFQIRLALTKQVQQYD"
gene                 4291. .5781
                     /gene="recS"
CDS                  4291. .5781
                     /gene="recS"
                     /function="DNA repair and homologous recombination"
                     /note="similar to Escherichia coli recQ gene product;
                     putative"
                     /citation=[3]
                     /codon_start=1
                     /transl_table=11
                     /product="DNA or RNA helicase, DNA-dependent ATPase"
                     /protein_id="AAC83947.1"
                     /db_xref="GI:1146200"
                     /translation="MTKLQQTLYQFFGFTSFKKGQQDIIESILSGKDTIAMLPTGGGK
                     SLCYQLPGYMLDGMVLIVSPLLSLMEDQVQQLKARGEKRAAALNSMLNRQERQFVLEH
                     IHRYKFLYLSPEALQSPYVLEKLKSVPISLFVIDEAHCISEWGHDFRPDYSKLGQLRK
                     KLGHPPVLALTATATKETLQDVMNLLELQHAVRHLNSVNRPNIALRVENAADTAEKID
                     RVIQLVENLQGPGIVYCPTRKWAKELAGEIKSKTSSRADFYHGGLESGDRILIQQQFI
                     HNQLDVICCTNAFGMGVDKPDIRYVIHFHLPQTAEAFMQEIGRAGRDGKPSVSILLRA
                     PGDFELQEQIIQMESVTAEEIADVIRVLEKTEERDERRLRDVLLQYGVGETQARMMIH
                     LFMQGKTSVELMKKEISYRMELKLEKMHRVSFLLQRDGCLRQALLTYFDESYEPDDGN
                     LPCCSHCGFDLSLYEQKGERSKMAPLDSWSSELHRIFSLQTVGELN"
gene                 5841. .6410
                     /gene="ypbD"
CDS                  5841. .6410
                     /gene="ypbD"
                     /note="putative"
                     /citation=[3]
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAC83948.1"
                     /db_xref="GI:1146201"
                     /translation="MTQLLIIFAAAAAGLFFFEDVRDVLKLWDIRDMRIIWYGVSIAV
                     IVILADMAVMKWFPSHLYDDGGINKKIFSKRSIPHIIFLTLLIAFAEEMLFRGVLQTH
                     IGLWTASLIFAALHFRYLSKWLLFIMVTAISFLLGLMYEWTGNLFVPMTAHFIIDAVF
                     ACQIRFEHVRRDKHDEHVESREKKSPESL"
gene                 6361. .7083
                     /gene="ypbE"
CDS                  6361. .7083
                     /gene="ypbE"
                     /note="putative"
                     /citation=[3]
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAC83949.1"
                     /db_xref="GI:1146202"
                     /translation="MTNMSRVERRKAQNLYEDQNAALADDDYVDDGESLPTRQSVKNQR
                     EQKKKQGKTKTPLFTVLAVIFVFVPVIVLVTLFYLKSHPDNHDDYEDVFIDSSQSKYE
                     VVPKSEDKNDTADTKETALQKESKKEPEDSKPKEQTAADKKQTAVAEKEDSPNKEEAT
                     AAAASSSQSTVQQQEQPAEPVQNVPNRVVKHTVQKKETLYRISMKYYKSRTGEEKIRA
                     YNHLNGNDVYTGQVLDIPLMDE"
gene                 7146. .7589
                     /gene="ypbF"
CDS                  7146. .7589
                     /gene="ypbF"
                     /note="putative"
                     /citation=[3]
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAC83950.1"
                     /db_xref="GI:1146203"
                     /translation="MESLWNQLDQFTDAPTKQMLQALVKRKQKFENYAAQCRRWRWAS
                     LICLGLLCVMIMIKSPEPQLILQEILSHTFYLFWMLATAFAYCTSYYFKKKEEKSETD
                     FHKLRCEIIQKSTDLWPQPDKWKARESVFHMMKHKYDINLYFESK"
terminator           7597. .7619
                     /note="putative"
                     /citation=[3]
gene                 7675. .8454
                     /gene="ypbG"
CDS                  7675. .8454
                     /gene="ypbG"
                     /note="putative"
                     /citation=[3]
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAC83951.1"
                     /db_xref="GI:1146204"
                     /translation="MKLSVKIAGVLTVAAAAMTAKMYATAKGNHLKTHTFPLSKMKGK
                     PPLTIFFISDIHKRLIDQDLLEKARSHAPHLVIIGGDLAEGGVPSARIEENIKRLVHF
                     GVPIVFVWGNNDYEVRQHKLYSIFKAHGVITLRNESVPFSYNGHTIAIAGVDDIRMEM
                     DHYEEAIKELDESQLNILVCHNPEIHEQINEDDGIDVILSGHTHGGQIRFGKFGPYEL
```

```
Query Match          51.3%;  Score 198.4;  DB 1;  Length 24887;
Best Local Similarity  71.2%;  Pred. No. 6.7e-35;
Matches  262;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy        20 AAAATGAGAAACAACTGCATCTAACAAGTCACCAAGACCTAAACCATGTGACCCTGATAT 79
             ||||||     |||| ||||| |  || ||||| || || |  || |||| || || ||
Db     21672 AAAATGCTCTGCAACGGCATCCAGTAAATCACCCAGTCCGAGTCCGTGTGTTCCCGAAAT 21613

Qy        80 CGGATACGGTTCACCAAATCCTAATGAATAGAAATCATACACGTCTGTACGCATTTCCAT 139
             |||||||| || ||||| |||| ||||| |||||||| | | | | ||||||  |
Db     21612 TGGATACGGCTCGCCAAAGCCTAGCGAATAAAAATCATAAATATTCGCTCTCATTTCTGT 21553

Qy       140 ATTATCTACTTTGTTAACCGCTAATACGACCGGTTTTTTAGATTTGTATAAAATTTGAGC 199
             ||||| | ||| |||||||||||| || || || ||||| |    ||| |||||||  ||
Db     21552 GTTATCCAGTTTATTAACCGCTAAAACAACAGGCTTTTTTGTGCGGTACAAAATTTTCGC 21493

Qy       200 GACCATTTCATCGCTTTGTGTCAATCCTTCACGCACGTTAACCATAAAAATAATAACATC 259
             ||   ||||||      |||||  |||||||  |||| ||||||||||||||| || ||
Db     21492 CACTTCTTCATCAGCAGCTGTCACGCCTTCACGGCCGTTCACCATAAAAATAATCACGTC 21433

Qy       260 CGCTTCATCTATGGCGATTTCTGCCTGCGCTCTAATTTGTGTTTGGAATGGTGCATCACC 319
             ||||||||| |||||||||| || |||   | ||| || | |   || ||  |||||||
```

```
Db      21432 CGCTTCATCCATGGCGATTTCAGCTTGCTGGCGAATCTGCGCTAAAAACGGCTCATCACC 21373

Qy        320 AATTTCAATACCACCTGTATCAATAATATTGAAATCATGTGTTAACCATTCACCTGAAGA 379
              || |||||||| || |||||||| | ||| |||||||    | | ||||||| | ||
Db      21372 GATATCAATACCGCCCGTATCAATCAAATTAAAATCATAATTCAGCCATTCAGCCGAGCT 21313

Qy        380 ATAAATAC 387
                || || |
Db      21312 GTATATCC 21305
```

Search completed: September 12, 2003, 19:27:28
Job time : 1589.02 secs